

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GGGCCCCGGG GGGCGGATTT TGTCTGCTT TGATTGTCCG TGGGATAAC GCGGTGATG	60
GTGCTAACCG CCGGATGGGC GGGCTGGCG GGGCTGGCG CCCCCCGCG GCGGCGGCG	120
TGATCAGCTT GCTGGGCGGC CAAGGCGCG GCGGGGCGCG CCGGACCGGC GGGGCGGCG	180
GTGTTGGCG TGACGGCGCG GCGGCGGCG CCGGCAACCA GCGCTTCAAC GCAGGTGCG	240
GCGGCGGCG CCGCTGATC AGCTGCTG GCGGCAAGG CCGGCGGCG GCGGCGGCG	300
CGGCGGCG CCGGCTGTT GCGGTGAC	329

(2) INFORMATION FOR SEQ ID NO:164:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GCAACGGTGG CAACGGGCG ACCAGCAGCA CCGTGGGAT GCGGAGGT AACTGTGTG	60
CGCGGGGCT GATCGCAAC	80

(2) INFORMATION FOR SEQ ID NO:165:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGCTGTGTC GCACTCACAC GCGGCAATC GCGACGTTG GCGGCAAT ATCCAGCTCA	60
AGGCTTACTA CTTACCGTC GAGGACCGC GCTCAAGGT GCGGTCAGC GCGCAAGGAA	120
TCAAGGTCAT CAGCGCGAC GCGATCGAG GCGTCTGTC GCGGCTGCG GCAGGATCG	180
CGCGGCGCA CTTGCGGCG CAAGCGGCT CATGCTGCG AACGCGGCG ATCTGTGAG	240
CACAACTGAT GCGGCGCAAC GAGATTCGTC CAATTGTCAA GCGTGTTCG ACCGAGGGA	300
CGGTTATAC GTATGTCAC CTATGTCAT CCGAAGAAC GCGATAACGA TCCGTGATC	360
CGCGACAGC CCACGAGTC AAGACCTTA CA	392

(2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

ACCGGCGCCCA CCGGCGGCAC CCGGTTCCGC GTTGCGCGCG GCGGGGCGCG CCGGCAGGGC      60
GGTATCAGCG GTGCGCGCGG CACCAACCGC TCTGGTGGCG CTGCGCGCAC CCGCGACAA      120
GGCGGCGCGG GGGCGGTGG CCGGCGCGGC GCGGATACCC CCACCGGCAT CCGCGCGCGC      180
GGCGGCACCG GCGGCACCGG CCGAGCGCGC GGAGCGCGCG GCGCGCGTGG CGGCATCGGT      240
ACCGGCGCCCA CCGGCGCGGC GTTGCGCAGC CTCGCTAACG CCGGGATCGG CGGTACCGGC      300
GGTACCGGTG GTGCGGTGG TGCTGGTGGT GCAGGTGGCG CTGCGCGCGC TGGCAGCAGC      360
CGTACCGGTG GCGCGCGGTT CCGCGCGCGC GCGCGCGGAG AAGCGCGACG GCGCGCGAAC      420
ACCGGTGTGG CCGGCACCAA CGGTCCCGC GCGCGCGCGG GTCCAGCGCG CAAGCGCGCG      480
ACCGAGGTG CCGGCGGTG CCGGCGCGAC AACCGACCG GTGCTGGTGT CCGCG      535

```

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

CCGACGTGGC CCGGCGGATA CCGGCGTCAC CGACTACTAC ATCATCGGCA CCGAGAATCG      60
GCGGTGTGGT CAACCGGTGC GCGCGGTGGC GTTCATCGGA GATCGGTGG CCGACGTGAT      120
CCAGCGGAAC CTGAAGGTGA TCTCAACCT GCGCTACGCG GACCGGAAT ACCGCTACTC      180
GACGAGCTAC GCGGATGTGC GAACGCGGT CCGGCTGTGG CCGAAGGTGC CGCTCAGGT      240
CATCGCGGAT GCGGTGGCG CCGGAACACA AGAAGGCATC CTTGACTTCA CCGCGGACCT      300
GCAGGCGGTG TCGCGCAAC CGCTCAGGT CCGCGAGATC CAGGTGGCGC AACCGCGGCA      360
TCTGGTGGCG GCGGTGGCG CCGCAACGAC GCGGCGGAG GTGGTGAACA CGCTCGCCAG      420
GATCATCTCA ACCAACTAG CGGTCTGCT GCGGACGTT GACATCGGCG TCGCTGGTTC      480
ACCAAGCTGC CGCTGTACAC CACCAACTG TTGCTAGGC AACTCGGTGC GCGCAATCTG      540

```

ATCAACGCGA TCGGCTATCC CCTGCGCGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG	600
CGGCGTGGAA TTGCTCAGCC TCCTCGCGGC GCGCTCGGAC ACCGTTGGAA ACATCGAGGG	660
CCTCGTCACC TAACGGATTC CCGACGGCAT	690

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACGCTGACCG CGGTACTGGC GCGCGCACG GCGGCAACG CGGGAATCC GGTGCGCTCT	60
TGGGCACAGC CGGGGTGGC GCGACGCTG GCGCCGCGAG CACCGTACT GCAGGTGGCG	120
GCTCTGGGGG CACCGCGGCG GACGCGCGA CCGCGCGCG TGGCGGCTG TTAATGGCG	180
CGCGCGCGCG CGGGACGGT GCGACTGGC GCGCGGCGG TCGCGGTCT GACCGTGGCG	240
GCGCGCGCGG GCGCGCGCG GCGCGCGCA ACGCGGCGC CGGGGTCAA GCGCGGCTG	300
TGTTGGGGCG CGGGCGACT GCGCGAGCG GCGGTACCG CGCGGTGGC GGTGGCGCG	360
GTGACGGCTT CGACGCGCG ATGCGCGCG TGGGTGGTAC CGGTGGC	407

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTGCG CGTCTCACCG AAGAACATCG	60
TGCACGCGGC GCGCGCGACC AGCGCGTTC GCTGCGGCG GTGGAACGCG TCGAGCAGGC	120
ACAGCCAGTC CTGCGCGGCG TCGAGCGCA ACAGCTCGGT CTCACCGGTG TAGATCGGCG	180
GGATGCGGCG CTCGCGCAAC GCATTGCGCG ACGCGCGCG GTCTTTGTGA TGCTCGACGA	240
TCACCGCGAT GTCTGCGGCG ACCACGCGCG GCGCGCGAA GGTGCGCGCG CTGCGCAGTA	300
GCGCGCGGAC GTCGCGCGCG AGGTGCTCG GGATGTGCGG GCGCAGCGGT CCGCGCGGAC	360
GCGCGAAAAA CGACCGCTCA CCGAGTGGG TCGCGGTGCG ATATCGCTTG CCGTCTGCG	420
CGATATTGGA CGCGCATGCC CCGACTGCGT ACAGCGCGCG CAGCAGCG	468

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

GGTGGTAACG GCGGCCAGGG TGGCATGCGG GCGGCCGCGG AGAGAGGCGC CGACGGCGCC      60
GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC      120
GGCGGGCGCG GCGGCAATGG GCGCGCGGGG GCGAACGCGC AGCGGGCGCG GTACACCGAC      180
GGCGCCACCG GCACCGCGCG CGACGGCGGG AACGGCGGCG

```

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

TAGCTCGCGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GCGGTGACG GCGTCGGCGG      60
CAACAGTTCC CTCACCCAGG GCGGCAGCGG CGGTGGCGGC GCGGCCGCGG GCGCTGGCGG      120
CAGCGGCTTT TTGGCGGCGA AGGGCGGCTT CCGCGGGGAC GCGGTGACG GCGGCCCGAA      180
CGCGGGCGGT ACCGTGGCGA CGGTGGCGCG TGGCGCGCGC AACGGCGGTG TCGGGCGGCG      240
GGCGGGCGAC GCGGTCTTTG CCGGTGGCGG CGGCCAGGCG GCGCTCGGTA GCGAGGGCGG      300
CAATGGCGCG GGTTCACCGG GCGGCAACGG CGGCTTTGCG GCGCGGGCGG CTGGCGGAGG      360
CAACGGCGCG GCTGTGGCGG AATCGGGGCT GACCATGGAC AGCGCGGCGA AGTTGGCTGC      420
CATCGCATCA GCGCGGTACT GCGCGGAACA CCGGAACAT CACCGGAGTT AGCGGGCGCG      480
ATTTCCTGAT CAGC

```

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

GGGCGCGTGG TGCCCGCGGC CAGCTCTTCA GCGCCGAGG CGCGCGCGGT GCCGTTGGGG      60
TTGCGCGCAC CGCGCGCCAG GGTGCGGCTG GCGGTGCGCG AGCGCGCGGC GCGGACGCGC      120
CGCCGAGCAC AGGTCTAACC GTGTGTACCG GTTTCGCTGG CGCGCGCGGC GCGGTGCGCG      180
GCCGAGCGCG CAACGCGATT GCCGCGCGCA TCAACGCGTC      220

```

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

ATGCGCGCAA CGCGCGCGCG GCGCGTGTG GCGCGCGCGG CGACTACAA TTCCAAACGG      60
GGGCAGGCTG GTGCGCGCGG CCAAGCGCGC CAAGCGCGCG TTGCGCGCGC AAGCACCACG      120
TGATCGGCGT AGCGCGCGCG GCGAAAGCG ATCCAAACAG CGACGATGCG GCCTTCTTGG      180
CGCGCTTGGG CCAAGCGCGG ATCACTTACG CTGACCGAGG CCACGCGATA ACGCGCGCGA      240
AGCGCATGTG TGGCTGTGT GCTAACCGCG TAACAGGTCT ACAGCTGCTC GCGGACCTGC      300
CGGACTACAA TTGCGGCTG ACCATGGAAC GCGCGCGCGA GTTCGCTGCG ATCGCATCAG      360
GCGCTTACTG CCGCGAACAC CTGGAACA      388

```

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

GCAGAGGCGG CACCGCGCGG GCGCGCATGA ACAGCTCGA CCGCTGCTA GCGCGCGAAG      60
ACGCGCGCGA AGCGCGCACC GCGCGCACC GCGCGAACGC CGCGCGCGGC GGCACCGAGT      120
TCACCCAGG CCGCGACGGC AAGCGCGCGA ACGCGCGTGA CCGCGCGGTC GCGCGCAACG      180
CGCGAAACGG CCGAAACGGC GCAGACAACA CCACCGCGGC CGCGCGCGGC ACCACAGGCG      240
GCGACCGCGG GCTGCGCGCG GCGCGCGGAA CCGCGCGAAC CCGCGGAGCT GCGCGCACCG      300
GCACCGCGCG CCAACAAGGC AACGCGCGCA ACGCGCGCAC CCGCGCGGAA GCGCGCACCG      360

```

GGGGGACCGG TGCACCTCTCA GGCAGCACCG GTGGTCCCGG

400

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 518 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCAACGGCG GCAACGGCGG CATCCCGGGC ATTGGGCGGC AACGGCGTTC CCGGACGGCG	60
AGCGGCAACG GCGGCCAAGC GCGGCACCGG CCGCAACGGC GGCACCGCGG GCATCGGCGG	120
CAACAGCGGC ACCGGCAGCG GCGACCGCGG TCGCGGCGGG AACCGCGCGG CCGCGGCGAC	180
GGCGGCGCAC GCGCGCGAGG GCGGCGTCCG CGTACTGGC GGCACCGCGG GCAGCGGTGG	240
CACCGCGCGT GACCGCGGTA ACCGCGGCGA CCGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGCGCGGC GTGACGGTG GCAACCGCGG CGACGCTGGC TTCGGCGCGG GCGCGCGCGC	360
CGCGCGCGGT GCGTTGACCG CTGGCGCCAA CCGCACCGGC GGCACAGCGG GCGCGCGCGG	420
GCATGCGCGC AACCGCGCGA TCGCGCGCGA CCGCGCGACTE ACTGACGACC CCGCGCGCAA	480
CGGGGCGCAC GCGCGCAAGC GCGGCACCGG CCGCACCGGC GCGCGCGCGA TCGCGCAC	518

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGGCGCGTGG TCGCGCGGGC CAGCTCTTCA GCGCGCGAGG CCGCGCGGGT GCGGTTGGGG	60
TTCGCGCGAC CCGCGCGCGG GTGCGCGCTG CCGGTGCGCG AGCGCGCGCG GCGGACGCGC	120
CGCGCGCGAC AGGTCTAACC GTTGGTACCG GTTTCGCTGG CCGCGCGCGG GCGGTCGCGG	180
GCCACGCGCG CAACGCGCATT GCGCGCGCGA TCAACGCGTC CCGTGGTGGC GCGCGCAC	219

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 988 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGCAGCGCTA CCGGTGGCGC CCGGTTCCGC GCGCGCGCCG GCGGAGAAGG CCGAGCGGGC	60
GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGCGGGCG CCGGCGGTGC AGGCGGCAAG	120
GGCGGCACCG GAGGTGCGCG CCGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCGCGG GCGGCACAGG TGGCGCGGGC GCGCGCGGGG GGGCGGCGCG GCGGACCGGT	240
ACCGGCGGCA CCGCGCGGCT TGTGCGCGCG ACCGGTAGTG CAGGCATCGG CCGGCGCGGC	300
GGCGCGCGCG GTGACGGCGG CGATGGGCGG AGCGGTCTCG GCCTGCGGCT CTCCGCGTTT	360
GACGCGCGCG AAGCGCGGCA AGCGCGGGCG GCGCGCAGCG CCGGCGCGCG CCGCATCAAC	420
GGGCGCGCGG GCGCGCGCGG CAACGCGGGC GACGCGCGGG AGGCGGCAAC CGGTGCGGCA	480
GGTGTGCGCG ACAACGCGGG GTTCGCGGCT GACGGTGGGG CCGGTGCGCG CCGCGGCAAC	540
GGCGGCAACG CCGCGGTGCG CCTGACAGCG AAGCGCGGCG AGGCGGCGCG CCGCGGCAAT	600
GGCGGCAACG GGGCGCGCGG CGGTGCTGCG GCGCGCGGCG ACAACAATTT CAACGCGCGC	660
CAGGTGTGTC CCGCGCGGCA AGCGCGGCAA GCGCGCTTGG GCGGCGCAAG CACCACTGCA	720
TGGCGGTAGC CCGACCGCGG AAAGCGGATC CAACAGCGCA CGATGCGGCG TTCCTTGCGG	780
CGTTGGAACA GCGCGGATC ACGTACGCTG AGCGAGGCGA CCGCATAAAG GCGCGCAAGG	840
CGATGTGTGC GCTGTGTGCT AACCGGTAA CAGGTCTACA GTGCTGCGCG GACCTGCGGG	900
AATACAATCC CCGGCTGACG ATGACAGCGC CCGGCAAGTT CGCTGCGATC GCATCAGCGG	960
CGTACTGCGG CGAACACTTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:178:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CGGCACGAGG ATCGGTACCG CCGGCGATCG GCAGCTGCGG ATTGCGCGCG TTTCCCGACC	60
CGAGGAAAGC CGGTACCAGA TGGCGCTGCG GAAGTAGGGC GATCGGTTCG CGATGCGGCG	120
ATGAACGCGG GGCATCAAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGC AGGATGATCC GATATGACCG ACTGCGAGAC CGTGACGCTG GATCAGGAG	240

AGATTTTGA	CAGGGCCAC	GAGGTGGAGG	CCCCGATGGC	GGACCCACCG	ACTGATGTCC	350
CCATCACACG	GTGGAACTC	ACGGCCGCTA	AAAACCCCGC	CCAACAGCTG	GTATTGTCCG	360
CCGACAACAT	GGGGAAATAC	CTGGCCGCGG	GTGCCAAAGA	GCGGCAGCGT	CTGGCGACTT	420
CGCTGCGCAA	CCCGGCCAAG	GCGTATGGCG	AGGTTGATGA	GGAGGCTGCG	ACCGCGCTGG	480
ACGACGACCG	CGAGGGAAT	GTGCAGGCAG	AATCGGCCCG	GGCGGTCCGA	GGGGACACTT	540
CGGCGGAAT	AACCGATAAG	CCGAGGCTGG	CCACCGCCCG	TGAACCCAAC	TTCATGGATC	600
TCAAAGAAGC	GGCAAGGAAG	CTCGAAACCG	GCGACCAAGG	CGCATCGCTC	GCGCACTTTG	660
CGGATGGGTG	GAACACTTTC	AACCTGACCG	TCCAAGGCGA	CGTCAAGCGG	TTCCCGCGGT	720
TTGCAACTG	GGAAGGCGAT	GCGGCTACCG	CTTGCGAGGC	TTGCGTCGAT	CAACAACGCG	780
AATCGATACT	CCACATGCGC	AAATTGAGCG	CTGCGATGGC	CAAGCAGGCT	CAATATGTCC	840
CGCAGCTGCA	CGTGTGGGCT	AGCGCGGAAC	ATCCGACTTA	TGAAGACATA	GTCCGGCTCG	900
AACGGCTTTA	CCCGGAAAAC	CGTTCCGCCC	GCGACCAAT	TCTCCCGGTG	TACGCGACT	960
ATCAGCAGAG	GTCCGAGAAG	GTGCTGACCG	AATACAACAA	CAAGGCAGCC	CTGGAACCGG	1020
TAAACCGCGC	GAAGCCTCCG	CCCGCCATCA	AGATCGACCC	GCCCCCGGCT	CCGCAAGAGC	1080
AGGATTTGAT	CCCTGCGTTC	CTGATGCGCG	CGTCTGACCG	CTCCGGTGTG	ACTCCCGGTA	1140
CCGGATGCGC	AGCGGCACCG	ATGCTTCGCG	CTACCGGATC	GGCGGTTGCT	GGCTTCCCGG	1200
CTGACACGCG	GCGGCAGCTG	ACCTCGGCTG	GCGCGGAAGC	CGCAGCGCTG	TCGGGCGACG	1260
TGGCGTCAA	AGCGGCATCG	CTCGGTGGCG	GTGGAGGCGG	GGGGGTGCGG	TCGGCGCGCT	1320
TGGGATCCCG	GATCGGGCGC	GCGGAATCGG	TGCGGTCGCG	TGGCGTGGCT	GACATTCGCG	1380
GCTTAGGCCA	GGAAGGGCGC	GCGCGCGCGC	CGCGCTGCGG	CGCGGTTGCG	ATGGGAATGC	1440
CGATCGGTGC	CGCGCATCAG	GGACAGGGCG	GCGCCAACTC	CAAGGTTTCT	CAGCAGGAAG	1500
ACGAGGCGCT	CTACACCGAG	GATCGGGCAT	GGACCGAGGC	CGTCATTGGT	AACGTCGCGC	1560
CGCAGGACAG	TAAGGAGTCC	AAGTGAGCAT	GGACGAATTG	GACCGGCATG	TCGCGCGCGC	1620
GTTGACGCTG	GCGGCGCGGT	TTCAGTGGCG	CCTAGACGGG	ACGCTCAATC	AGATGAACAA	1680
CGGATCTTTC	CGCGCCACCG	ACGAACCGCA	GACCGTCGAA	GTGACCATCA	ATGGGCACCA	1740
GTGGCTCAAC	GGCTTGCGCA	TGGAAGATCG	TTTGCTGAAG	AAGCTGGGTG	CGGAGCGCGT	1800
GGCTCAGCGG	GTCAACGAGG	CGCTGCACAA	TGCGCAGGCG	GCGGCGTCCG	CGTATAACGA	1860



```

CGCGGCGGGC GAGCAGCTGA CCGCTGGCTT ATCGGCCATG TCCCGCCCA TGAACGAAGG 1920
AATGGCTTAA GCGCATTTGT GCGTGGTAG CGACTACGCA CCGAATGAGC GCGSCAATGC 1980
GGTCATTCAG CGCGCCCGAC ACGCCGTGAG TACGCTTGT CAATGTTTTT ACATGGATCG 2040
GCGGGGTTCC GAGGGCGCCA TAGTCTGGT GCGCAATATT GCGGCAGCTA GCTGGTCTTA 2100
GGTTCGGTTA CGCTGGTTAA TTATGACGTC GGTACCA 2118

```

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
35           40           45
Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100          105          110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115          120          125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130          135          140
Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
145          150          155          160
Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
165          170          175
Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
180          185          190

```

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln  
 195 200 205  
 Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro  
 210 215 220  
 Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro  
 225 230 235 240  
 Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg  
 245 250 255  
 Ser Gln Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro  
 260 265 270  
 Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro  
 275 280 285  
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser  
 290 295 300  
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met  
 305 310 315 320  
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala  
 325 330 335  
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp  
 340 345 350  
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val  
 355 360 365  
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg  
 370 375 380  
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly  
 385 390 395 400  
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala  
 405 410 415  
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu  
 420 425 430  
 Asp Glu Ala Leu Tyr Thr Gln Asp Arg Ala Trp Thr Glu Ala Val Ile  
 435 440 445  
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:180:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Ala	Gly	Asn	Val	Thr	Ser	Ala	Ser	Gly	Pro	His	Arg	Phe	Gly	Ala	Pro	1	5	10	15
Asp	Arg	Gly	Ser	Gln	Arg	Arg	Arg	Arg	His	Pro	Ala	Ala	Ser	Thr	Ala	20	25	30	
Thr	Gln	Arg	Cys	Arg	Phe	Asp	Arg	His	Val	Ala	Arg	Gln	Arg	Cys	Gly	35	40	45	
Phe	Pro	Pro	Ser	Arg	Arg	Gln	Leu	Arg	Arg	Arg	Val	Ser	Arg	Gln	Ala	50	55	60	
Thr	Thr	Arg	Arg	Ser	Gly	Arg	Arg	Asn	His	Arg	Cys	Gly	Trp	His	Pro	65	70	75	80
Gly	Thr	Gly	Ser	His	Thr	Gly	Ala	Val	Arg	Arg	Arg	His	Gln	Glu	Ala	85	90	95	
Arg	Asp	Gln	Ser	Leu	Leu	Leu	Arg	Arg	Arg	Gly	Arg	Val	Asp	Leu	Asp	100	105	110	
Gly	Gly	Gly	Arg	Leu	Arg	Arg	Val	Tyr	Arg	Phe	Gln	Gly	Cys	Leu	Val	115	120	125	
Val	Val	Phe	Gly	Gln	His	Leu	Leu	Arg	Pro	Leu	Leu	Ile	Leu	Arg	Val	130	135	140	
His	Arg	Gln	Asn	Leu	Val	Ala	Gly	Arg	Arg	Val	Phe	Arg	Val	Lys	Pro	145	150	155	160
Phe	Gln	Pro	Asp	Tyr	Val	Phe	Ile	Ser	Arg	Met	Phe	Pro	Pro	Ser	Pro	165	170	175	
His	Val	Gln	Leu	Arg	Asp	Ile	Leu	Ser	Leu	Leu	Gly	His	Arg	Ser	Ala	180	185	190	
Gln	Phe	Gly	His	Val	Gln	Tyr	Pro	Leu	Pro	Leu	Leu	Ile	Glu	Arg	Ser	195	200	205	
Leu	Ala	Ser	Gly	Ser	Arg	Ile	Ala	Phe	Pro	Val	Val	Lys	Pro	Pro	Glu	210	215	220	
Pro	Leu	Asp	Val	Ala	Leu	Gln	Arg	Gln	Val	Glu	Ser	Val	Pro	Pro	Ile	225	230	235	240
Arg	Lys	Val	Arg	Gln	Arg	Cys	Ala	Leu	Val	Ala	Arg	Phe	Glu	Leu	Pro	245	250	255	

Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His  
 260 265 270

Pro Arg Arg Ile Gly  
 275

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg	Val	Ala	Ala	Ser	Phe	Ile	Asp	Trp	Leu	Asp	Ser	Pro	Asp	Ser	Pro	1	5	10	15
Leu	Asp	Pro	Ser	Leu	Val	Ser	Ser	Leu	Leu	Asn	Ala	Val	Ser	Cys	Gly	20	25	30	
Ala	Glu	Ser	Ser	Ala	Ser	Ser	Ser	Ala	Arg	Ser	Gly	Asn	Gly	Ser	Arg	35	40	45	
Trp	Thr	Ser	Met	Pro	Ser	Gly	Thr	Arg	Pro	Gly	Pro	Arg	Arg	Ala	Thr	50	55	60	
Ser	Arg	Asp	Asp	Arg	Arg	Ser	Ala	Thr	Ser	Val	Ile	Pro	Ser	Arg	Arg	65	70	75	80
Ser	Val	Ala	Pro	Arg	Ala	Glu	Phe	Gly	Thr	Arg	Leu	Ala	Ser	His	Arg	85	90	95	
Ala	Ser	Pro	Ser	Asn	Ala	Cys	Pro	Val	Arg	Ile	Val	Thr	Ser	Ala	Ser	100	105	110	
Gly	Arg	Pro	Ile	Ser	Ser	Pro	Pro	Ile	Val	Arg	Ser	Arg	Ser	Cys	Val	115	120	125	
Asp	Lys	Asn	Gly	Arg	Arg	Cys	Ala	Ser	Gly	Tyr	Arg	Arg	Leu	Asn	Arg	130	135	140	
Ala	Arg	Ser	Ser	Ser	Ile	Ala	Ala	Arg	Cys	Arg	Thr	Ile	Gly	Thr	Phe	145	150	155	160
Arg	Arg	Ser	Arg	Tyr	Ser	Ala	Ser	Met	Arg	Val	Ser	Thr	Asn	Ser	Pro	165	170	175	
His	Val	Thr	His	Gly	Val	Ala	Pro	Gly	Val	Thr	Arg	Arg	Ile	Gly	Gly	180	185	190	

(2) INFORMATION FOR SEQ ID NO:182:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Gln Ile Glu Pro Arg
1           5           10           15

Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
          20           25           30

Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro
          35           40           45

Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val
          50           55           60

Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala
          65           70           75           80

Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln
          85           90           95

Ala Gly Arg Val Arg Arg Gly Gln Gln Leu His His Arg His Arg His
          100          105          110

Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val
          115          120          125

Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val
          130          135          140

Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His
          145          150          155          160

His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly
          165          170          175

Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val
          180          185          190

Gly Gly Ser Ala
          195

```

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Val	Arg	Cys	Gly	Thr	Leu	Val	Pro	Val	Pro	Met	Val	Glu	Phe	Leu	Thr	1	5	10	15
Ser	Thr	Asn	Ala	Pro	Ser	Leu	Pro	Ser	Ala	Tyr	Ala	Glu	Val	Asp	Lys	20	25	30	
Leu	Ile	Gly	Leu	Pro	Ala	Gly	Thr	Ala	Lys	Arg	Trp	Ile	Asn	Gly	Tyr	35	40	45	
Glu	Arg	Gly	Gly	Lys	Asp	His	Pro	Pro	Ile	Leu	Arg	Val	Thr	Pro	Gly	50	55	60	
Ala	Thr	Pro	Trp	Val	Thr	Trp	Gly	Glu	Phe	Val	Glu	Thr	Arg	Met	Leu	65	70	75	80
Ala	Glu	Tyr	Arg	Asp	Arg	Arg	Lys	Val	Pro	Ile	Val	Arg	Gln	Arg	Ala	85	90	95	
Ala	Ile	Glu	Glu	Leu	Arg	Ala	Arg	Phe	Asn	Leu	Arg	Tyr	Pro	Leu	Ala	100	105	110	
His	Leu	Arg	Pro	Phe	Leu	Ser	Thr	His	Glu	Arg	Asp	Leu	Thr	Met	Gly	115	120	125	
Gly	Glu	Glu	Ile	Gly	Leu	Pro	Asp	Ala	Glu	Val	Thr	Ile	Arg	Thr	Gly	130	135	140	
Gln	Ala	Leu	Leu	Gly	Asp	Ala	Arg	Trp	Leu	Ala	Ser	Leu	Val	Pro	Asn	145	150	155	160
Ser	Ala	Arg	Gly	Ala	Thr	Leu	Arg	Arg	Leu	Gly	Ile	Thr	Asp	Val	Ala	165	170	175	
Asp	Leu	Arg	Ser	Ser	Arg	Glu	Val	Ala	Arg	Arg	Gly	Pro	Gly	Arg	Val	180	185	190	
Pro	Asp	Gly	Ile	Asp	Val	His	Leu	Leu	Pro	Phe	Pro	Asp	Leu	Ala	Asp	195	200	205	
Asp	Asp	Ala	Asp	Asp	Ser	Ala	Pro	His	Glu	Thr	Ala	Phe	Lys	Arg	Leu	210	215	220	
Leu	Thr	Asn	Asp	Gly	Ser	Asn	Gly	Glu	Ser	Gly	Glu	Ser	Ser	Gln	Ser	225	230	235	240
Ile	Asn	Asp	Ala	Ala	Thr	Arg	Tyr	Met	Thr	Asp	Glu	Tyr	Arg	Gln	Phe	245	250	255	
Pro	Thr	Arg	Asn	Gly	Ala	Gln	Arg	Ala	Leu	His	Arg	Val	Val	Thr	Leu	260	265	270	
Leu	Ala	Ala	Gly	Arg	Pro	Val	Leu	Thr	His	Cys	Phe	Ala	Gly	Lys	Asp	275	280	285	

Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp  
 290 295 300

Arg Asp Val Ile Val Ala Asp  
 305 310

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTCTTCCCGA TTGGGCACGA GCTGAGCAGC CCAAGGGGCG GTTCGGGCGAA GTCATCGAGG	60
CATTGCGCGA CCGGCTGGCC GGCAAGGGTA AGCAANTCAA CACCACGCTG AACAGCTTGT	120
CGCAGGCGTT GAACGGCTTG AATGAGGGCC GCGGCGACTT CTTCGGGCTG GTACCCAGCC	180
TGGGCTATT CTTCAACGCG CTACATCAGG ACCACCAACA GTTCGTCCCG TTGAACAAGA	240
ACCTTCCGGA GTTCACCGAC AGGTTGACTC ACTCCGATGC GGACCTGTCC AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCGTCCGCGC GCGGCTTCTT CCGCAAGAAC CGCGAGGTGC	360
TGACGCATGA CTTCAATGAT CTGCGACCGG TGACCAACAC GTTGCTGCAG CCGGATCCCT	420
TGGATGGGTT GGAGACGCTC CTGCACATCT TCCCGACGCT GCGCGCGAAC ATTAACCCAGC	480
TTTACCATCC GACACACGCT GCGGTGGTGT CCGTTTCCGC GTTCACGAAT TTGCGCAACC	540
CGATGGAGTT CATCTCCAGC TCGATTCCAG CCGGTAGCCG GCTCGGTTAT CAAGAGTCCG	600
CGGAAGTCTG TCGCAGTAT CTGGGCGCAG TCGTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTGGGCTT GAACGTGGCC AGCAGCGGCT CGACACTGCG TAAAGAGATC GGTACTTCCG	720
AGCGCGGCTT GCAGCGCGCC AACGGGTACA AGGACACCAC GGTGCGCGGC ATCTGGGTGC	780
CGGATACGCT GTTGTCAACG CGCAACACCG AGCGCGGTTG GGTGGTGGCA CCGGGGATGC	840
AAGGGGTTCA GGTGGGACCG ATCAGCGCAG GTTTGCTGAC GCGCGAGTCC CTGGCGGAAC	900
TGATGGGTGG TCGGATATC GCGGCTCGCT CGTCAGGGCT GCAAAACCCG CCGGGACCCC	960
CGAATGCGTA CGAGGATAC CCGGTGCTGC CCGGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCGGCTTCTT GGGCGGACCG TAATCCCGGG TCGGTGCGCA CCGGTCTTGG	1080
CGCGATGCTT GTTCCCAAGA GATCGCGCGG CAGCGTCCGA AAACCTCCAC TACATGGGCC	1140

TCTTGTTCCT	GTGCGCGGCG	CTGGCGACCT	TCCTTTTCGG	GGTGTGATCT	AGCCCCGCCC	1280
GTGGAACGAT	GGCTGATCGG	CACCTGTTGA	TACCGGCGAT	CACCGGCGTG	GCGTGTGATG	1280
CGGCATTGCT	CGCACATTGG	TGGTACCGCA	CAGAACATCC	GCTCATAGAC	ATGCGCTTGT	1320
TCCAGAACCG	AGCGGTGCGG	CAGGCCAACA	TGACGATGAC	GGTGCTCTCC	CTCGGGCTGT	1380
TTGGCTGCTT	CTTCTGCTTC	CCGAGCTACC	TCCAGCAAGT	GTTGCACCAA	TCACCGATGC	1440
AATCGGGGCT	GCATATCATC	CCACAGGGCC	TGGTGGCCAT	GCTGGCGATG	CCGATCGGCC	1500
GAGCGATGAT	GGACCGACCG	GGACCGGCCA	AGTCTGTGCT	GGTTGGGATC	ATGCTGATCG	1560
CTCGGGGGTT	GGGCACCTTC	GCTTTTGGTG	TGGCGCGGCA	AGCGGACTAC	TTACCGATTC	1620
TGCGGACCGG	GCTGGCAATC	ATGGGCGATG	GCATGGGCTG	CTCGATGATG	CCACTGTCCG	1680
GGCGGCGCAT	GCAGACCTCG	GCGCCACATC	AGATCGGCTG	CGGTTCGACG	CTGATCAGCG	1740
TCAACCGACA	GCTGGGGGCT	TGGATAGGGA	CGGCACTGAT	GTGGGTGCTG	CTCACCTACC	1800
AGTTCAATCA	CAGCGAAATC	ATCGCTACTG	CAAGAAAGT	CGCACTGACC	CCAGAGAGTG	1860
GGCGCGGGCG	GGGGCGGGCG	GTTGACCTTT	CTTGCTTACC	GCGCCAAACC	AACTTCGCGG	1920
CCCAACTGCT	GCATGACCTT	TGGCAGGCTT	AGCGGCTGCT	ATTGCTGATA	GCGACCGGCG	1980
TAGTGGTCTC	GACCGTGATC	CGCGCGGAT	TCTGCGGAA	ACAGCAGGCT	ACTCATCGAA	2040
GAGCACCCTT	GCTATCCGCA	TGACGTCTCC	TT			2072

(2) INFORMATION FOR SEQ ID NO:185:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCACCCCGGA	GAAGTCCTTC	GTGACCGACC	TGGACATCGA	CTGGCTGTCT	ATGGTCCAGA	50
TGGCGGTGCA	GACCGAGGAC	AAGTACGGCG	TCAAGATCCC	CGACGAGGAC	CTCGCCGGTC	120
TGGGTAGGCT	CGGTGACGTT	GTGGCTTACA	TCCAGAAGCT	CGAGGAAGAA	AACCGGAGG	180
CGGCTCAGGC	GTTGCGCGCG	AAGATTGAGT	CGGAGAACCC	CGATGCGGCA	CGAGCAGATC	240
GGTGCCTTTC	ACCCACATCG	CAAGCTTCGAC	AGCGCCGTCG	TCTTCTTGCA	CGCTCAGGCA	300
GGTTGGCGTG	TGGCGGCGTT	CGAGCAAGTG	TTCCACACAC	ACGAAGGAGC	CCTCGCGAAA	360
GGTGACTGAT	CGCGCGACCA	CATAGTCGAT	GCCACGCTGG	CTGACAAATG	CGCCGGGTTC	420



GAGTTGGCGG	GGGCCGAATT	GCGGCATTGC	GTGGAAGGCC	AGCGGATCCC	GGCGCCCGCC	480
CGCGGTGGCT	GCTTTTTTGG	GCGGCCGGAT	GCCGACGACG	AGAACGACCA	TGGCGCGGAT	540
GAACAGCGCC	ACGGCAATCA	CGACCAGCAG	ATTTCGCCACG	CATACCCCTCT	CGTACCGCTG	600
CGCGCGCGTT	GCTCGATCGG	TGCGATATCG	ATGGGCGCGT	TTAACGTAAAC	AGCTTTCCCG	660
CGACCGCGGG	TCACAACGGG	CGAGTTGTTC	GGCGCGGAAC	CGGCGAGGTC	TGCGCCCGCG	720
TCACCCCGAC	TCAGTGGTGC	ACCATCCGGG	TGTCGCTGAG	CGTGCNACTC	AAACACACTC	780
AACCGCAACG	GTTTCTCAGG	TCACCGAGTC	AACCTCGAAC	CGCAATCGCT	CGTACGTTTC	840
GACCGCGCGC	AGGTGCGGAG	TCAGCAGCTT	TGCGCCCGCA	GCTTTCCCGG	TGAAGCGGAC	900
CAGGGCATCG	TAGGTTCCGC	CACCGGTGAC	ATCGTGCTCG	GCGAGGTGCT	CGGTCAAGCC	960
GCGATATGAG	CAGGCATCCA	GTGCCAGGTA	GTTGCTGGAG	GTGATGTCCG	CCAAGTAGGC	1020
GTGACCGCGA	ACAGGGGCAA	TACGATCGGG	CGGTGCTAGC	CGGCTCAGCA	CGGAATAGGT	1080
TTCCACAGCC	GCCTGCGCGA	TCAGATGGAC	GCCACGCTTG	AGCGGCGCGA	CGCGCGGCTC	1140
GTGCGCTTCC	TGCGAGCTCG	CGAATCGCGC	AACCAGGACG	CTGGTGCTTG	GTGCGATCAC	1200
CGCGGTGTGC	GATCGAGCGT	TTCCCGAACG	ATTTCGTCCG	TCAACGCGCG	CAGGGGACGT	1260
TTGCGCGCTG	CGACGAGAAC	CGAGCGTTCC	CGAACGAGTT	CGACACCGGT	CGCGCCCGCG	1320
TCATCTCGCA	TGCGCCGATC	GCGTCCGCTG	ATCTCCACCT	GGTCCGTTCC	GCGCAAGCCA	1380
AGCGCGCTCG	GAATCCGCTT	GCGAATCACC	AGACGTCTTG	CGACATCGAT	GCTTGTTCGG	1440
ATGCTAGGAA	ATTTACCATC	GCACGTTCCA	TAGGCGTCTC	CTGCGCGCGA	TGTCGGGACG	1500
ATCGGCTAGC	GATCGGACG	ATTGTTTCCG	AAATGGCTGA	GCGAGCGTGC	GCTGCGGCTG	1560
ATGGGTGTTC	ATCCCGGGTT	GACCGGATGC	GGGCTGTGCG	TCATCGAGAG	TGGGCGTGGT	1620
CGGCAGCTCA	CGCGCGTGGG	TGTCGAGCTG	GTGCGCACAC	CGTCGGATGC	GCGCTTGGCG	1680
CAGCGCTGTG	TGGCATTCAG	CGATGCGCTC	GAGCACTGCG	TGGACACCCA	TCATCCGGAG	1740
GTGGTGCTCA	TCGAACGGGT	GTTCTCTCAG	CTCAACGTGA	CCACGGTGAT	GCGCACCGCG	1800
CAGCGCGCGG	GCTGATTCGC	CCTGCGCGCG	GCCAAACGTG	GTGTGAGCTT	GCAATTCCAT	1860
ACCGCCAGCG	AGGTGAAGGC	GCGCGTCACT	GCGAAGGCTT	CGCGAGACAA	GCTTCAGGTC	1920
ACC						1923

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

CTGGCGTGGC AGTGTACACC GCGATATGAC GTCCGGCATT AATTTCGCGG CCCCAGCGGA      60
CCCGTCGCCA CCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTCT CCAAGTGGGT      120
GCCCAATGTT GTCTGGGTT TCTTGAACGA AGGCCTGCGG TATCGGGTGC CTAACCCCA      180
AACAAGCGCA GTCCAGGAAT CCGGTCCCGC GCGGCGGATY CCGAGCGGA TGTCTAGCC      240
GGCGATGGTT CAGACGTAA CTTTGGGTAG GTCGAAACCC GCGCCAGGCG CCGTGGACCG      300
GCTCATGGCA CGGAATTAG AAAACTCGCG ATATTGTCCG CGGATTGTCA TACGATGCTG      360
AGTCTTGGT GGTTCGTGTT TAGCCATGGA GTGTGATGT GTTGAGACCC TGGCCTGSA      420
GGGACAACG TGCTTTTCC TCTTGGTCCG CTTTTCGCGC CCGACGCGGT GGTGGCGAAA      480
CGGCTGAGT CCGGAATGCT CGCGCGCTTG TCGTTTCGCG TCAGCTGGCG AGTGGCTGTG      540
CCACCGGATG ATTATGACCA CTGGCGGCTT GCGCCGAGG ACGGCGCGCA TGTGGATGTC      600
CAGGCGGCGG AAGCGCGCGA CCGAGAGGCT GCGGCCATCG ACCAGTGGGA TGAGTGGCAG      660
CGTGGGAAG AGTGGGTGGC GGAGAACGCT GAACCGGCT TTGAGGTGGC ACCGAGTAGC      720
AGCAGCGTGA TTCCGCATTC TCGCGCGCGC GGTAGGAGA GCGGCGCGAG ACTGTGCTTA      780
TTTGACCAAT GATCGCGCGT CTCGTGTTT CCGCGCGCGG CTATGACAA CAGTCAATGTG      840
CATGACAACT TACAGGTATT AGGTCCAGCT TCAACAAGCA GACAGGCAAC ATGSCAACAC      900
GTTTTATGAC GATTCGCGAC GCGATCGCGG ACATGCGCGG CCGTTTTGAG GTGCACGCCC      960
AGACGGTGGG GACGAGGCT CCGCGGATGT GGGCTCGCGC GCRAAACATC TCGGGGCGCG      1020
CGTGGAGTGG CATGCGCGAG GCGACCTGCG TAGAC      1055

```

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

CGGCTTCGTT GTTGGCATA TCGCGCGCGG CCGCTCGGAC CGCAATGCGC GTGGGCTGTG      60

```

```

TCCGCGCTGA CCACCGGGAT CCGCGAACCA TCCGAGATCA CTTGCGAATG ATCCACCTCG      120
CCGAGCTGGT CACCCAGCCA CCGCGCGGTG TCGGACAGCG CTTGCATCAC CTGCGTATAG      180
CCGTCGCGCC CCGCGCGCAG GAAGTTGTAG TACTGCCCCA CCACCTGGTT ACCGCGACCG      240
GAGAAGTTCA GGTGAAGGT CCGCATGTGG CCGCGAGGT ACTTGACCGG GAAAACCAGA      300
TCTTCGCGCA GTGCTCGGG CCGCGCCAC AGGACAAACC CGACGCGCG ATAGGTCAG      359

```

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

AACCGGCCCC TCGGCACCGC TCTCTAAGG GCTCTCGTTG GTGCGATGAA GTGCTGGAAG      60
GATGCATCTT GGCAGATTCC CCGCAGACA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC CTCGAATAAC TCGTACCGG GAGGCCCCAA CCGGCTCTCC TTCGCTAAGC      180
TCCGCGAACC ACTTGAGGTT CCGCGACTCC TTGACCTCCA GACCGATTGG TTCGAGTGGC      240
TGATCGGTTG GCGCGCTGG CCGCAATCCG CCGCGAGCG GGTGATGTC AACCCAGTGG      300
GTGCGCTGGA AGAGGTGCTC TACGAGCTGT CTCGATCGA GGACTTCTCC      359

```

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

Glu Glu Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp      1
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Glu Ile Asn Thr Thr Leu Asn Ser Leu      20
20          25          30
Ser Glu Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala      35
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Glu Asp Asp      50
50          55          60

```

Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Gln Phe Thr Asp Arg  
 65 70 75 80  
 Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp  
 85 90 95  
 Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val  
 100 105 110  
 Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Thr Leu Leu  
 115 120 125  
 Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro  
 130 135 140  
 Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly  
 145 150 155 160  
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe  
 165 170 175  
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser  
 180 185 190  
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys  
 195 200 205  
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr  
 210 215 220  
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Glu Pro Pro Asn  
 225 230 235 240  
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro  
 245 250 255  
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met  
 260 265 270  
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu  
 275 280 285  
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser  
 290 295 300  
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro  
 305 310 315 320  
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro  
 325 330 335  
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu  
 340 345 350  
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe

385	390	395
Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu 370 375 380		
Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His 385 390 395 400		
Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val 405 410 415		
Ala His Ser Trp Tyr Arg Thr Gln His Pro Leu Ile Asp Met Arg Leu 420 425 430		
Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu 435 440 445		
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln 450 455 460		
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro 465 470 475 480		
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met 485 490 495		
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile 500 505 510		
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp 515 520 525		
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met 530 535 540		
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala 545 550 555 560		
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln 565 570 575		
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr 580 585 590		
Gln Phe Asn His Ser Gln Ile Ile Ala Thr Ala Lys Lys Val Ala Leu 595 600 605		
Thr Pro Gln Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser 610 615 620		
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser 625 630 635 640		
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser 645 650 655		

Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg  
 660 665 670

Arg Ala Pro Leu Leu Ser Ala  
 675

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser  
 1 5 10 15  
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile  
 20 25 30  
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala  
 35 40 45  
 Tyr Ile Gln Lys Leu Glu Glu Gln Asn Pro Glu Ala Ala Gln Ala Leu  
 50 55 60  
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg  
 65 70 75 80  
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala  
 85 90 95  
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr  
 100 105 110 115  
 Thr Arg Arg Asp Pro Arg Glu Arg  
 115 120

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg  
 1 5 10 15  
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser

	20		25		30										
Ile	Ala	Glu	Gly	Arg	Gln	Val	Arg	Ala	Gln	Cys	Gly	Ala	Gly	Phe	Leu
	35					40						45			
Glu	Arg	Arg	Pro	Ala	Val	Ser	Gly	Ala	Leu	Pro	Pro	Asn	Asn	Ala	Ser
	50					55				60					
Pro	Gly	Ile	Arg	Ser	Arg	Ala	Ala	Asp	Ser	Gln	Arg	His	Leu	Leu	Ala
	65				70					75					80
Gly	Asp	Gly	Ser	Asp	Val	Thr	Val	Gly							
					85										

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ala	Ser	Leu	Leu	Ala	Tyr	Ser	Ala	Ala	Ala	Ala	Ser	Thr	Ala	Leu	Ala
1				5						10				15	
Val	Ala	Cys	Val	Arg	Ala	Asp	His	Arg	Asp	Arg	Arg	Thr	Ile	Arg	Asp
			20					25					30		
His	Leu	Ala	Met	Ile	His	Leu	Ala	Gln	Leu	Val	Thr	Gln	Pro	Pro	Gly
	35						40					45			
Gly	Val	Arg	Gln	Arg	Leu	His	His	Leu	Gly	Ile	Ala	Val	Ala	Pro	Gln
	50					55				60					
Pro	Gln	Glu	Val	Val	Val	Leu	Ala	His	His	Leu	Val	Thr	Gly	Thr	Gly
	65				70					75				80	
Glu	Val	Gln	Gly	Glu	Gly	Arg	His	Val	Ala	Ala	Glu	Val	Val	Asp	Pro
			85					90						95	
Glu	Asn	Gln	Ile	Leu	Arg	Gln	Val	Leu	Gly	Pro	Ala	Pro	His	Asp	Lys
			100					105						110	
Pro	Asp	Ala	Gly	Ile	Gly	Gln									
			115												

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu  
 1 5 10 15  
 Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Glu Ser Lys Thr Ala  
 20 25 30  
 Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val  
 35 40 45  
 Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu  
 50 55 60  
 Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu  
 65 70 75 80  
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val  
 85 90 95  
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile  
 100 105 110  
 Glu Asp Phe Ser  
 115

## (12) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGGTACGCGAG CAATCGCTTT GGTACAGAT GTGGATGCGG GCGTCGCTGC TGGCGATGCG 60  
 GTGAAAGCCG CCGACTGTTT CCGCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG 120  
 GTGCGGGGCG CCAATCGATCG GTTCGCGGAC GAGCGCACCT GCACGCACTG TCAACAGCAC 180  
 GCGGTGTGTC GTTTCGCTT CAGCTGCGA TGAGGCTGCT GCTGACCGGC GCGGCGCGCT 240  
 TCATCGGGTC GCGGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTGG 300  
 AGCGGTGCTT GCGGCGCGCG CACGCGCGCA ACCCGTGTCT GCGACCGCGC TCGCAGCGGG 360  
 TCGACGTGCG CAGCGCGAGC GCGGTGCGCG CTTTGTGCGC CGGTGTGAT CTGCTGTGTC 420  
 ACCAGCGCGC CATGTGCTT GCGGCGCTCA ACCCGCGCA CCGACCGCGC TATGCGCGCC 480  
 ACAACGATTT CCGCAGCAGG GTGCTGCTGG CGCAGATGTT CCGCGCGCGG GTCCGCGCTT 540



```

TGGTGTCTGGC GTCGTGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG      600
GACCGGTGCA CCGCTTCCCG CGGCGGCCAG CCGACTTGA CAATGGGCTC TTCGAGCACT      660
GTTCCCGCGG GTGCGGCCAG CCACTCATCT GGCAATTGGT CGACGAAGAT GCGCCCTTTC      720
GCCCCCGCAG CTTGTACCGG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC      780
GGAAACGAAT GCGCGTTCCG TGGTGGCCTT G              811

```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

GTCCCGCGAT GTGCGCGAGC ATGACTTTGG GCAACACCGG CGTAGTAGTC GAAGATATCG      60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTGGG GTTGGTCAGC GTCACCCGTT      120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTGCG TCACACAAGT CGCGAGCGTA      180
ACCTCACCGT CAAATATCGC GTGGAATTTC GCGTGCAGT TCCGCTCGCG GACAATCAAG      240
GCATACTCAC TTACATGCCA GCCATTTGGA CGGTTTCGAT CGCTTTCGGG CTGGTGAACG      300
TCCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCAGC      360
CCAGCGACAA CGGACCGATC CATTACAGC GCGTCTGCGA GCGGTGTGGC GAGGTGXTCC      420
ACTACCGCGA TCTTGGCCCG GCTACGAGT CCGCGCAGCG CCMAATGGTG GCGATCACCG      480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCCGGA GATCGAGGTC TTGGAGTTCC      540
TCCCGCGCGC CGACGTGGAC CGGATGATGT TCGACCGCAG CTACTTTTTC GAGCCTGATT      600
CGAAGTCTGC GAAATCGTAT GTCTGCTGCG CTAAGACACT CGCGAGACC GACCGGATCG      660
CGATCGTGA TCGCCCGAGC GCGCTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT      720
TCGCGCTCGA GTTCGGCTAC CACAAACGGT AGAAGGATCG AGACATTCCC GAGCTGAAGT      780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AATACGCTT ACTCATGCCA      840
TGGGCGCTGC TCACCGGATG CGACGTTTTT GCCACGCTCC ACCGCTGCG GCGCGACCTC      900
AAGTGGGCAT GCATCCGAGC GTTTCCCGGA AACCGGTTCC GCGCGTCCG CTCATCGCTT      960
CATCGT              966

```

(2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

CCGCACCGCC GGCATACCG CCAGCGCCAC CGTTACCGCC GTTTCGCGCC TTGCCCCCGT      60
TGCCTCCCGT CCGCGCGGCC CCGCGGATGG ACTTCTCATC GCGAAAAGTA CTGCGCTTGC      120
CAGCGGAGGC GCGGTTGCGG CGGTACCGCC CAGCCCCGCC GACTCCACCG GCGCCACCGA      180
CTCCGCGCGT GCCACCGTTG CCGCGGTTGC CGATCAACAT GCGGCTGGCG CCACCGTTGC      240
CAGCCACCGT ACCGCGTGGC CCGACCGCGC CGACACCAAG CGAGCTGCGG CCGGAGCCAC      300
CATCAGCAGC TACGCCACCG ACCGCCGAGA CAGCAGCGAC CGGCTCTTGC TGAACCTCTC      360
CGGTGCGCAC ACCGCGCGCG TTACCGCCAA CCGCACCGGC AACGCGCGCG CCGCCATCGC      420
CGCGCGCGCG GCGGTTGCGG CGGTGCGCGC GGTTCGCGAA CAACAACCGG CCGCGCGCGC      480
CGTTGCGCGC CCGCGCGCGG GTCCGCGCGG CCGCGCGCAC GCGAAGGCGG CTGCGCGCGT      540
TGCGCGCATC ACCACCGTTG CCGCGGAGCA CATCGGGTTC TGCGTCGGGG TCTGCGCTGT      600
CAAACCTGCG GATGCCAGCG TTGCGCGCGC TTGCGCGCGG CCGCGCGCGT GCGCGCTCAC      660
CAGCGGAGCG ACCGCGCGCA CCGCGCGCAC CGTTGCGCGC ATCAGCGAAT AGCAACCGCG      720
CGCGCGCGCG ATTGCGCGCA GGTGCGCGTG CCGCACCGTC GCGCGCGGAG CCGGCACTGG      780
CAGCGCGCGT ACCACCGAAA CCGCGCGCTAC CACCGGTAGA GTGCGCAGTG GCGATGTGTA      840
CGAAGCGCGC GCGTCGCGCG CCGCGCGCTAC CACCGCGACT GCGCGCGGCT ACACCGTGGG      900
ACCGCTTGGC ACCATCACCG CCAAGGCGCG TCGCATGTTC GCGGTGCGCG ACTCGCGCGT      960
CGCGCGCGTT CCGCGCGCGG CCACCGCGCG CCGCGGTACC GCGGTACCA CCGGCACCGC      1020
CGGTGCGCGT CCGCGAGCGT GCGGTGCGCG TGCGACCGTC GCGCGCGGTG CCACCGGTGG      1080
GCGTGCAGCG AGTGCCATGG CCGCGCGTGC CCGGTGCGCG GCGCGTTTGA TCACCGATGC      1140
CGGACACATC TGCGCGCGTG TCGCGCGTGC TGCGCGCGCG GCGCGCGGTG GCGATGACCG      1200
CGTTTGCGCG GCGGAGGCGG GCGCGCGCGG TACGACCGCG GCGCGCATGG CCGAACAGCG      1260
CGCGGTGCGC GCGGTTACCG CCGGCACCGC CGATGCGTGC GCGCACCGTG GTGCGCGCGA      1320
CAGCGCGCGT GCGCGCGTTG CCGCACCAAG ACTCGCGCGT CCGACCGCGA CCGCGCGCGG      1380

```

```

CGCCGGTACC ACCGCCCCCG CCGTTGCGCG CCGTTGCGGAT CAGCCCGGCC GCGCTTCGCG 1440
TCCCGCGCGT TTGACCGAAC CCGCCAGCGG CCGCGTTGCG ACCGTTGCGA AACAGCAACC 1500
CGCCGCGCGC GCGAGGCTGC CCGCGTGGCG TCCCGTCGCG GCGGTTTCGG ATCAGCGGGC 1560
GCCCCAAAG CCGCTCGGTG GCGCATTCA CCGCAGCCAG CAGACTCGCG TCAACAGCGG 1620
CTTCAGTGGT GGCATACCGA CCGCGCGCGG CAGTCAACGC CTGCACAAAC TGCTCGTGAA 1680
ACGCTGCCAC CTGTACGCTG AGCGCTGAT ACTGCCGAGC ATGGGCGCGG AACAAACCGG 1740
CAATCGCGCG CAGACTTCA TCGGCAGCGG CAGCCAGCAC TTCCGTGCTC GGCATCGCGG 1800
CGCGCGGATT AGCGCGCTC ACCTCGAAC CAATAGTCCA TAAATCCAA GCGCGAGTTC 1860
CGAGCAGCTG CGCGTGGCG ATCAGCAAGG ACACCTCGCA CCGCGGATA CCGCATATCG 1920
CGCAGCGCTG TCGCAGCGG CCGCGTGGCG TTGCGTGGCT GCGTGGCGCG CCGTACTATG 1980
GCGCGAGCGG CCGTCTTCT GATTGCGCGG GCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040
GGGAGGACAG GCGAGCTTG CTGTAGAGCT GCGTCAAGT GGAATGACG GTCCCGCGCG 2100
AGATGAATAG GCGGAGCGCG ATCTCTTCT TCGTAGTTC CTCACCGACC AGTAGAGCCA 2160
CGTCAAGCTC TGTCGGTCT AACGCGCGCG AGCGACTTCT CCGCGGTTTC CCGTACCGCG 2220
GCGCTCGTTG CGGTAGCGG ATCGGCTCAT CGATCGATAA CGCAGTTCTT TCGCGCGAGG 2280
CATCGTCGAA CTGCTGTCA CCGATGGATT TTGGAAGGT GCGTAGCGAC GAGTTACAGC 2340
CGCGCTGTA GATCCGGAAG CGAGCTC 2367

```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
1           5           10           15

Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
20           25           30

Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
35           40           45

Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
50           55           60

```

Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp  
 65 70 75 80  
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr  
 85 90 95  
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg  
 100 105 110  
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala  
 115 120 125  
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly  
 130 135 140  
 His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly  
 145 150 155 160  
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly  
 165 170 175  
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr  
 180 185 190  
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala  
 195 200 205  
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala  
 210 215 220  
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg  
 225 230 235 240  
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala  
 245 250 255  
 Thr Val Ala Lys Glu Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys  
 260 265 270  
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu  
 275 280 285  
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe  
 290 295 300  
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu  
 305 310 315 320  
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser  
 325 330 335  
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser  
 340 345 350

Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg  
 355 360 365

Ala His Leu Arg Thr Asn Ser Arg  
 370 375

(2) INFORMATION FOR SEQ ID NO:198:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

GGCCAAAACG CCCCCGCGAT CCGCGCCACC GAGCGCGGCTT ACCACCAGAT GTGGGCCCGAG      60
GACGTGGCGG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGCCCGTCTC GGCTTTGACA      120
CGTTTCGCGC AGGCGCTGCC GACCGTGGCG GCGCGCGGTC CGCTGCTCAG CCGCGCCGCG      180
GCTCAGGTGA CCACGCGGCT TTCCGCAAC CTGGGCTTGG CGACGTCCG CGACGGCAAC      240
GTCCGCAACG STAATGTCCG GAACCTCAAT CTCGGCTCGG CCAACATCGG CAACGGCAAC      300
ATCGGCAGCG GCAACATCGG CAGCTCCAAC ATCGGTTTGG GCAACGTGGG TCGTGGGTTG      360
ACCGCAGCGC TGAACAACAT CGGTTTGGCG AACACCGGCA GCAACAACAT CGGTTTGGCG      420
AACACCGGCA GCAACAACAT CGGTTTGGCG AATACCGGAG ACGGCAACCG AGGTATCGGG      480
CTCAGCGGTA GCGTTTGTGT GGGGTTCCGC GGGCTGAAT CCGGCACCGG CAACATCGGT      540
GTGTTCAACT GGGGCACCGG AAAGTTCGCG ATCGGCAACT CCGGTACCGG GAAGTGGGCG      600
ATTGGCAACT GGGGCAACAG CTACAACACC GTTTTTGGCA ACTCCGGGCA CCGCAACACG      660
GGCTTCTTCA ACTCGGGAAT AGCCAACACC GGGCTCGGCA ACCCGGGCAA CTACAACACC      720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GGGGCTTCA ACATGGGCCA GTACAACACC      780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGGTTGGGCA ACTCGGCAAA TGTCAACACC      840
GGCGGCTTCA TTAAGGGCAA CTTCACAAAC GCTTTCTTGT GCGCGGGGCA CCACCAAGGC      900
GTGATTTTGG GGAGCGCGCG GTTCTTCAAC TCGACCAAGT GCGCGTCTC GCGATTCTTC      960
AACAGCGGTC CGGTAGCGCG GTCCGGGTTT CTGAACCTCG GTGCCAACAA TTCTGGCTTC      1020
TTCAACTCTT GTTCGGGGGC CATCGTTAAC TCGGGGCTTG CAAACGGCGG CGTGCTGGTA      1080
TCGGGCGTGA TCAACTCGCG CAACACCGTA TCGGTTTGT TCAACATGAG CCGGGTGGCG      1140
ATCACAACGC CGGCTTTGAT CTCGGGCTTC TTCAACACCG GAAGCAACAT GTCCGGATTY      1200

```

TTGGGTGGGC	CACCGGTCTT	CAATCTGGGC	CTGGCAAAAC	GGGGGCTGCT	GAACATTCTC	1260
GGCAACGCCA	ACATCGGCAG	TTACAACATT	CTCGSCAGCG	GAAACCTGCG	TGACTTCAAC	1320
ATCCTTGGCA	CGCGCAACCT	CGGCAGCCAA	AACATCTTGG	GCAGCGGCAG	CGTCGGCAGC	1380
TTCAATATCG	GCAGTGGAAA	CATCGGAGTA	TTCAATGTGG	GTTCGGGAGG	CCTGGGAAAC	1440
TACAACATCG	GATCGGAAA	CCTCGGAGTC	TACAACATCG	GTTCGGGAAA	CGTCGGGAGC	1500
TACAACATCG	GCTTCGGGAA	CGCGGGGAGC	TTCAACCAAG	GCTTTGCCAA	CACCGGCAAC	1560
AACAACATCG	GGTTGGGCAA	CACCGGCAAC	AACAACATCG	GCATCGGCTT	GTTCGGGAGC	1620
AACCGAGAGG	GCTTCAATAT	TGCTAGCGGC	TGGAATCTCG	GCATCGGCAA	CAGCGGCTTC	1680
TTCAATTCGG	GCACCAATTA	CCTTGGCAGC	TTCAACGGCG	GCACCGGAAA	CGTCGGCAGC	1740
GCAAACTCGG	GCACCGGGAA	CTGGGGTATC	GGGAACCGCG	GTACCGGCAA	TACCGGAGTC	1800
CTCAATGCTG	GCAGCTACAA	CACCGGAGTC	CTCAACGGCG	GGGACTTCAA	CACCGGCTTC	1860
TACAACACGG	GCAGCTACAA	CACCGGAGTC	TTCAACCTCG	GTAACACCAA	CACCGGCAAC	1920
TTCAACCTCG	GTGACACCAA	TACCGGAGTC	TATAACCGCG	GTGACACCAA	CACCGGCTTC	1980
TTCAATTCGG	GCACCTGCAA	TACCGGAGTC	TTCAACACGG	GGGACTTCAA	CAATGGCTTC	2040
TTGGTGGCGG	GGGATAACCA	GGGCGAGATT	GGGATCGATC	TCTGGGTGAC	CATTCGATTC	2100
ATCGGCTTAA	ACGAGGAGAT	GCTCATTTGAC	GTACACAGCG	TAATGAGCTT	CGGCGGCAAC	2160
ATGATCAGCG	TCACCGAGGC	CTCGAGCTTT	TTGCGGCAAA	CCTTCGATCT	GAGCGGTTTTG	2220
TTCTTTCTCG	GGCGGTGCAA	TCTCAGGCGA	TCCAGGCTGA	CGTTTCGAGC	GATCAGCTTC	2280
ACGATCGGCG	GACCGAGCTT	GACCGTCTCT	ATCAGGATTC	TGGGTGCTCT	GGGAGGCGCG	2340
ACGATGAGCT	TCTTCAAGAT	CGATCGGCGC	CGCGGAGTCG	GAAATTCGAG	CACCAAGCTTC	2400
TCTTCGCGCT	TCTTCAAGAT	GGGCAAGCTT	GGCAATCTCG	GCTTCGAAA	CGTCGGGCGC	2460
GGCAGTTGAG	GCTTCTGGAA	CAGTGGTTTTG	AGCAGGCGGA	TAGGGAATTC	GGGTTTCGAG	2520
AACCTCGGCT	CGTTCAGATC	AGGCTGGGCG	AACCTGGGCA	ACTCGGATTC	GGGTTTTTTTC	2580
AACACCAATA	CGGTGAAGCT	CTCCAGGCGC	GGCAATGTCT	CGGCGCTGAA	CAACATCGGC	2640
ACCAAGCTGT	CGGCGTGTCT	CGGCGGTGCG	ACCGGAGCGA	TTTTCAAGCG	GGGCTTTGCC	2700
AACCTGGGCG	AGTTGAACAT	CGGCAAGCGC	TGGTGGCGAA	TTGGGAGCGA	GTTAGATAGC	2760
GTTCGAACAA	TCATATCGCG	GTTCGGGCGC	AGTGCATCAG	ACCAATCGAA	CGGCGGAAAC	2820

GTAAGCGAAT AAACCGAATG GCGGCTGTTC AT

2853

## (3) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Gly	Gln	Asn	Ala	Pro	Ala	Ile	Ala	Ala	Thr	Glu	Ala	Ala	Tyr	Asp	Gln	1	5	10	15
Met	Trp	Ala	Gln	Asp	Val	Ala	Ala	Met	Phe	Gly	Tyr	His	Ala	Gly	Ala	20	25	30	
Ser	Ala	Ala	Val	Ser	Ala	Leu	Thr	Pro	Phe	Gly	Gln	Ala	Leu	Pro	Thr	35	40	45	
Val	Ala	Gly	Gly	Gly	Ala	Leu	Val	Ser	Ala	Ala	Ala	Ala	Gln	Val	Thr	50	55	60	
Thr	Arg	Val	Phe	Arg	Asn	Leu	Gly	Leu	Ala	Asn	Val	Arg	Gln	Gly	Asn	65	70	75	80
Val	Arg	Asn	Gly	Asn	Val	Arg	Asn	Phe	Asn	Leu	Gly	Ser	Ala	Asn	Ile	85	90	95	
Gly	Asn	Gly	Asn	Ile	Gly	Ser	Gly	Asn	Ile	Gly	Ser	Ser	Asn	Ile	Gly	100	105	110	
Phe	Gly	Asn	Val	Gly	Pro	Gly	Leu	Thr	Ala	Ala	Leu	Asn	Asn	Ile	Gly	115	120	125	
Phe	Gly	Asn	Thr	Gly	Ser	Asn	Asn	Ile	Gly	Phe	Gly	Asn	Thr	Gly	Ser	130	135	140	
Asn	Asn	Ile	Gly	Phe	Gly	Asn	Thr	Gly	Asp	Gly	Asn	Arg	Gly	Ile	Gly	145	150	155	160
Leu	Thr	Gly	Ser	Gly	Leu	Leu	Gly	Phe	Gly	Gly	Leu	Asn	Ser	Gly	Thr	165	170	175	
Gly	Asn	Ile	Gly	Leu	Phe	Asn	Ser	Gly	Thr	Gly	Asn	Val	Gly	Ile	Gly	180	185	190	
Asn	Ser	Gly	Thr	Gly	Asn	Trp	Gly	Ile	Gly	Asn	Ser	Gly	Asn	Ser	Tyr	195	200	205	
Asn	Thr	Gly	Phe	Gly	Asn	Ser	Gly	Asp	Ala	Asn	Thr	Gly	Phe	Phe	Asn	210	215	220	
Ser	Gly	Ile	Ala	Asn	Thr	Gly	Val	Gly	Asn	Ala	Gly	Asn	Tyr	Asn	Thr				

225	330	235	340
Gly Ser Tyr Asn Pro	Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly		
245	250	255	
Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu			
260	265	270	
Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe			
275	280	285	
Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly			
290	295	300	
Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe			
305	310	315	320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn			
325	330	335	
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly			
340	345	350	
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn			
355	360	365	
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro			
370	375	380	
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe			
385	390	395	400
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val			
405	410	415	
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly			
420	425	430	
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly			
435	440	445	
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly			
450	455	460	
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn			
465	470	475	480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly			
485	490	495	
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn			
500	505	510	
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr			
515	520	525	



Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly  
 530 535 540  
 Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu  
 545 550 555 560  
 Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly  
 565 570 575  
 Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn  
 580 585 590  
 Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr  
 595 600 605  
 Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly  
 610 615 620  
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn  
 625 630 635 640  
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr  
 645 650 655  
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp  
 660 665 670  
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly  
 675 680 685  
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn  
 690 695 700  
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn  
 705 710 715 720  
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr  
 725 730 735  
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr  
 740 745 750  
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr  
 755 760 765  
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe  
 770 775 780  
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro  
 785 790 795 800  
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln  
 805 810 815

Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser	
820 825 830	
Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly	
835 840 845	
Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr	
850 855 860	
Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly	
865 870 875 880	
Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn	
885 890 895	
Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys	
900 905 910	
Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe	
915 920 925	
Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu	
930 935 940	

## (2) INFORMATION FOR SEQ ID NO:200:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGATCCCAAT GGGCCATCAT CATCATCATC ACCTGATCGA CATCATCCGG ACC

83

## (3) INFORMATION FOR SEQ ID NO:201:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCTGAATTCA GGCCTCGGTT GCGCCGGGCT CATCTTGAAC GA

42

## (2) INFORMATION FOR SEQ ID NO:202:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGATCCTGCA GGCTCGAAAC CACCGAGCG T 31

(2) INFORMATION FOR SEQ ID NO:203:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T 31

(2) INFORMATION FOR SEQ ID NO:204:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT 33

(2) INFORMATION FOR SEQ ID NO:205:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTCGA 38

(2) INFORMATION FOR SEQ ID NO:206:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCGCATCCGA GCCACGTGCC CACAACGCC 30

(2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTTCATGGA TTCTCAGGCC GGTAAAGTCC GCTGCGG 37

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGCGGAATGG GACGCGCCCT GTAGCGCCGC ATTAAGCGCG GCGGCTGTGG TGTTACCGG 60

CAGCGTGACC GGTACACTTG CCAGCGCCCT AGCGCCCGCT CTTTTGCTT TCTTCCTTC 120

CTTCTCGCC ACCTTCGCCG GCTTTCCCG TCAAGCTCTA AATCGGGGCG TCCCTTTAGG 180

GTTCGGATTT AGTGGTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGTTTC 240

ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT 300

TTTAAATAGT GGACTCTTGT TCCAACTGG AACAACACTC AACCTATCTT CGGTCTATTC 360

TTTGGATTTA TAAGGGATTT TGCGGATTC GGCCTATTGG TTAAGAAATG AGCTGATTTA 420

ACAAAAATTT AACCGGAATT TTAACAAAT ATTAAGCTTT ACAATTTCAG GTGGCACTTT 480

TGCGGGAAAT GTCGCGGGA CCGCTATTTG TTTATTTTTT TAAATACATT CAAATATGTA 540

TGCGCTCATG AATTAAATCT TAGAAAACT CATCGAGCAT CAAATCAAC TCGAATTTAT 600

TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCGG TTTCTGTAAAT GAAGGAGGAA 660

AGTCACCGAG GCACTTCCAT AGGATGGCAA GATCCTGCTA TCGGTCTGCG ATTCGCACTC 720

GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA 780

AATCACCATG AGTGACGACT GAATCGGCTG AGAATGGCAA AAGTTTATGC ATTTCTTTTC 840

AGACTTGTTC AACAGGCCAG CCATTACGCT CCTCATCAAA ATCACTCCCA TCAACCAAAC 900

CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAGAGGAC 960

AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT 1020

TTTCACCTGA ATCAGGATAT TCTTCTAATA CTTGGAATGC TTTTTCTCG GGGATCGCAG 1080

TGGTGAGTAA	CCATGCATCA	TCAGGAGTAC	GGATRAAATG	CTTGATGCTC	GGAAGAGGCA	1140
TAAATTCCTT	CAGCCAGTTT	AGTCTGACCA	TCTCATCTGT	AACATCATTT	GCAACGCTAC	1200
CTTTGCCATG	TTTCAGAAAC	AACTCTGGCG	CATCGGGCTT	CCCATACAAT	CGATAGATTG	1260
TGGCACCCTG	TTGCCCCACA	TTATCGCGAG	CCCATTATA	CCCATATAAA	TCAGCATCCA	1320
TGTTGGAAAT	TAATCCCGGC	CTAGAGCAAG	ACGTTTCCCG	TTGAATATGG	CTCATAACAC	1380
CCCTTGTAAT	ACTGTTTATG	TAAGCAGACA	GTTTTATTGT	TCATGACCAA	AATCCCTTAA	1440
CCTGAGTTTT	CCTTCCACTG	AGCCTCAGAC	CCCCTAGAAA	AGATCAAGAG	ATCTTCTTGA	1500
GATCCTTTTT	TTCTGCGCCT	AATCTGCTGC	TTCCAAACAA	AAAAACCACC	GCTACCAGCG	1560
GTGGTTTTGT	TGCGCGATCA	AGAGCTACCA	ACTCTTTTTT	CGAAGGTAAC	TGGCTTCAGC	1620
AGAGCGCAGA	TACCAAAATC	TGTCCTTCTA	GTGTAGCGGT	AGTTAGGCCA	CCACTTCAAG	1680
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAAT	GGCTGCTGCC	1740
AGTGGCGATA	AGTCGTGTCT	TACCGGCTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1800
CAGCGGTCTG	GCTGAACCGG	GGTTCTGTGC	ACACAGCCCA	GCTTGGAGCG	AACGACCTAC	1860
ACCGAAGTGA	GATACCTACA	GGTGAGCTTA	TGAGAAAGCG	CCACGCTTCC	CGAAGGAGCA	1920
AAGCGGAGCA	GGTATCCGCT	AAGCGGCGCG	GTCCAAACAG	GAGAGCGCAC	GAGGGAGCTT	1980
CCAGGGGGAA	ACGCTGCTTA	TCTTTATAGT	CTGTGCGGCT	TTGCGCACCT	CTGACTTGAG	2040
CCTCGATTTT	TGTGATGCTC	GTCAAGGGGG	CGGAGCTTAT	GGAAAAACGC	CAGCAACCGC	2100
GCCTTTTATC	GCTTCTGTGC	CTTTTCTGTG	CCTTTTCTTC	ACATGTTCTT	TCTTGGCTTA	2160
TCCGCTGATT	CTGTGGATAA	GGTATTATCC	GGCTTTGAGT	GAGCTGATAC	CGCTCGCCGC	2220
AGCGGAAGCA	CCGAGCGGAG	CGACTCAGTG	AGCGAGGAAG	CGGAAGAGCG	CCTGATGCGG	2280
TATTTTCTGC	TTACGCATCT	GTGCGGTATT	TCACACCGCA	TATATGGTGC	ACTCTCAGTA	2340
CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGTATACACT	CCGCTATCGC	TAGCTGACTG	2400
GCTCATGGCT	GCGCCCCGAC	ACCGGCGAAC	ACCGCTGAC	GCGCCCTGAC	GGGCTTGTCT	2460
GCTCCCGGCA	TCCGCTTACA	GACAAGCTGT	GACCGTCTCC	GGGAGCTGCA	TGTGTCAGAG	2520
GTTTTACCGG	TCATCACCGA	AACGCGCGAG	GCAGCTGCGG	TAAAGCTCAT	CAGCGTGGTC	2580
GTGAAGCGAT	TCACAGATGT	CTGCTGTGTC	ATCCGCGTCC	AGCTCGTTGA	GTTTCTCCAG	2640
AAGCGTTAAT	GTCTGCTTTC	TGATAAAGCG	GGCCTGTTTA	AGGCGGCTTT	TTTCTGTTTT	2700

GCTCACTGAT	GCCTCCCTGT	AAGGGGGATT	TCTGTTGATG	GGGTAATGA	TACCGATGA	3760
ACGAGAGAGG	ATGCTCAGCA	TACGGTTTAC	TGATGATGAA	CATGCCCCGT	TACTGGAACG	3820
TTGTGACGGT	AAACAACTGG	CGGTATGGAT	GCGGCGGGAC	CAGAGAAAAA	TCACTCAGGG	3880
TCAATGCCAG	CGCTTCGTTA	ATACAGATGT	AGGTGTTCCA	CAGGGTAGCC	AGCAGCATCC	3940
TGGATGCAAG	ATCCCGAACA	TAATGGTCCA	GGCGCGTAC	TTCCGCTTTT	CCAGACTTTA	3990
CGAAACACGG	AAACCGAAGA	CGATTGATGT	TGTTGCTCAG	GTGCGAGACG	TTTTGCAGCA	3950
GCAGTCGCTT	CAGTTTCGGT	CGCTATCGGG	TGATTGATTC	TGCTAACCCAG	TAAGGCAACC	3120
CCGCCAGCCT	AGCCGGGTCC	TCAACGACAG	GAGCAGGATC	ATGCGCAGCC	GTGGGGCCGC	3180
CATGCCCGCG	ATAATGGCCT	GTTTCTCGCC	GAAAGCTTTG	GTGGCGGGAC	CAGTGACGAA	3240
GGCTTGAGCG	AGGGCGTGCA	AGATTCCGAA	TACCGCAGGC	GACAGGCGCA	TCATGCTGCG	3300
GCTCCAGCGA	AAGCGGTCTT	CGCGGAAAAT	GACCCAGAGC	GCTGCCCGCA	CTTGTCTTAC	3360
GAGTTGCATG	ATAAAGAAGA	CATCATAAAG	TGCGGCGAGC	ATAGTCATGC	CCCGCGCCCA	3420
CCGGAAGGAG	CTGACTGGGT	TGAAGGCTCT	CAAGGGGATC	GATCGAGATC	CCGGTGCTTA	3480
ATGAGTGAGC	TAACTTACAT	TAAATGCTTT	GGGCTCACTG	CCCGCTTTCC	AGTCGGGAAA	3540
CGTGTGCTGC	CAGCTGCATT	AATGAATCGG	CCAACCGCGG	GGGAGAGCGG	GTTTGCGTAT	3600
TGGGCGCCAG	GTTGCTTTTT	CTTTTCACCA	GTGAGAGCGG	CAACAGCTGA	TTGCGCTTCA	3660
CCGCTTGCGC	CTGAGAGAGT	TGCAGCAGGC	GCTCCACGCT	GGTTTGCGCG	AGCAGGCGAA	3720
AATCCTGTTT	GATGGTGGTT	AACCGCGGGA	TATAACATGA	GCTGTCTTCC	GTATCGTCGT	3780
ATCCCACTAC	CGAGATATCC	GCACCAAGCC	GCAGCGCGGA	CTCGGTAAAG	GCGCGCATTC	3840
CGCCGAGCGC	CATCTGATCC	TTGGCAACCA	GCATCGCAGT	GGGAACGATG	CCCTCATTCG	3900
GCATTTGCAAT	GTTTTGTGGA	AAACCGGACA	TGGCACTCCA	GTGCGCTTCC	CGTTCCGCTA	3960
TGGGCTGAAT	TTGATTGCGA	GTGAGATATT	TATCCGAGCC	AGCCAGAGCC	AGACGGCGCG	4020
AGACGAAACT	TAATGGGCCC	GCTAACAGCG	CGATTTGCTG	GTGACCGCAAT	GCGACCAAGT	4080
GCTCCACGCC	CAGTGGCGTA	CGCTCTTCAT	GGGAGAAAAAT	AATACTGTTG	ATGGGTGTCT	4140
GGTCAGAGAC	ATCAAGAAAT	AACGCGGGA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG	4200
CATCTGCTGC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACGCTTTCG	GCGAGAAGAT	4260
TGTGCACCGC	CGCTTTACAG	GTTTCAGCGC	CGCTTCGTTG	TACCATCGAC	ACCACCAAGC	4320
TGGCAGCCAG	TTGATCGGCG	CGAGATTAA	TGCGCGGAC	AATTTGCGAC	GGCGCTGCA	4380

GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACGACTG	TTGGCCCCGC	AGTTGTTTGT	4440
CCACCCCGTT	GGGAATGTAA	TTGAGCTCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT	4500
TCCGAGAAAC	GTGGCTGGCC	TGGTTCACCA	CGCGGGAAAC	GGTCTGATAA	GAGACACCGG	4560
GATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT	CACCAACCTG	AATTGACTCT	4620
CTTCCGGGCG	CTATCATGCC	ATACCGCGAA	AGGTTTTGCG	CCATTGGATG	GTGTCCGGGA	4680
TCTCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAAG	AGCCCACTAG	TAGGTTGAGG	4740
CCGTTGAGCA	CGCCCGCCGC	AAGGAATGGT	GCATGCCAAG	AGATGGCGCC	CAACAGTCCC	4800
CCGGCCACGG	GGCTTCCAC	CATACCCACG	CGAACAAG	CGCTCATGAG	CCCGAAGTGG	4860
CGAGCCCGAT	CTTCCCCATC	GCTGATGTGC	GCGATATAGG	CGCCAGCAAC	CGCACTGTGT	4920
CGCCCGCTGA	TGCGGGCCAC	GATCGCTCCG	GGCTAGAGGA	TGGAGATCTT	GATCCCGCGA	4980
AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGATAA	CAATTCCCGT	CTAGAAATAA	5040
TTTTGTTTAA	CTTTAAGAAG	GAGATATACA	TATGGGCCAT	CATCATCATC	ATCACGTGAT	5100
CGACATCATC	GGGACCGGCC	CCACATCCTG	GGAACAGGCG	CGCGCCGAGG	CGGTCCAGCG	5160
GGCGCGGGAT	AGCCTCGATG	ACATCGCGCT	CGTCTGGGTC	ATTGAGCAGG	ACATGGCCGT	5220
GGACAGCGCT	GGCAGATCA	CTTACCGCAT	CAAGCTCGAA	GTGTCTTTCA	AGATGAGGCC	5280
GGCCCAACCG	AGGGGCTCGA	AACCAACGAG	CGTTTCGCGT	GAAACGGGCG	CCGGCGCGCG	5340
TACTGTGCGG	ACTACCCCGG	CTTCTGCGCC	GGTGACCTTG	GCGGAGAGCG	GTAGCAGCGT	5400
GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	GGCTTTTCAC	GAGAGGTATC	CGAACGTGAC	5460
GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	CGGATTCGCG	CAGGCGCGCG	CCGGGACGCT	5520
CAACATTGGG	GCTTCCGACG	CTATCTGTGT	GGAAGCTGAT	ATGGCCCGCG	ACAAGGGGCT	5580
GATGAACATG	GCGTAGCCCA	TCTCCCTTCA	GCAGGTCAAC	TACAACCTGC	CCGGAAGTGA	5640
CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	GGCGGCCATG	TACCAGGCGA	CCATCAAAAC	5700
CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	CCCCGGCGTG	AACCTGCCCC	GCACCGCGGT	5760
AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	TGACACCTTC	TTGTTCACCC	AGTACCTGTC	5820
CAAGCAAGAT	CCCGAGGGCT	GGGSCAAGTC	GGCGGGCTTC	GGCACCACCG	TGACTTCCC	5880
GGCGGTGCGG	GTTGCGCTGG	GTGAGAACGG	CAACGGCGCG	ATGGTGACCG	GTTGCGCGGA	5940
GACACCGGGG	TGCGTGGCGT	ATATCGGCAT	CAGCTTCCTC	GACCAGGCCA	GTCACGGGG	6000

ACTGCGCGAG	GCCCACTAG	GCAATAGCTC	TGGCAATTTC	TTGTTGCCCC	ACGCGCAAG	6060
CATTGAGGCT	GCGCGGCTG	GCTTGGCATT	GAAAACCCCG	GCGAACCGAG	CGATTTCGAT	6120
GATCGACCGG	CCCCCCCCCG	ACGGCTACCC	GATCATCAAC	TACGAGTACG	CCATGCTCAA	6180
CAACCGGCAA	AAGGACGCGG	CCACCGGCGA	GACCTTGCGG	GCATTTCCTG	ACTGGGCGAT	6240
CACCGACCGC	AACAAGGCGT	CGTTGCTCGA	CCAGGTTGAT	TTCCAGGCGC	TGCGGCGCGC	6300
GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	GACGATTTCC	AGCGCTGAGA	TGAAGACCGA	6360
TGCCCTACCG	CTCGCGCAGG	AGGCAGGTAA	TTTCGAGCGG	ATCTCGCGCG	ACCTGAAAAC	6420
CCAGATCGAC	CAGGTGGAGT	CGACGCGAGG	TTCTTTGCGG	GCGCACTGCG	GCGGCGCGCG	6480
GCGGACGCGC	GCCGAGGCGG	CGGTGCTGCG	CTTCGAGGAA	GCAGGCAATA	AGCAGAAGCA	6540
GGAACCTGAC	GAGATCTCGA	CGAATATTGG	TCAGGCGCGC	GTCCATATCT	CGAGGCGCGA	6600
CGAGGAGCGG	CAGCAGGCGC	TGTGCTCGCA	AATGGGCTTT	GTGCGCACAA	CGCGCGCGTC	6660
GCGCGCGTGG	ACCGCTGCGG	CGCCACCGCG	ACCGGCGGCA	CCTGTTGCGC	CCCCACCGCG	6720
GCGCGCGCGC	AACACGCGCA	ATGCGCGCGC	GCGCGATCGC	AACCGAGCGC	CTCGCGCGCG	6780
CGACCTGAAAC	GCACGCGCGC	CACCTGTCAT	TGCGCGCAAC	GCACCGCAAC	CTGTCGCGAT	6840
CGACAACTCG	GTGCGAGGAT	TCAGCTTCGC	GCTGCGTGGT	GGCTGGGTGG	AGTCTGAGCG	6900
CGCGCACTTC	GACTAGCGTT	CAGCACTCGT	CAGCAAAACC	ACCGGGGACC	CGCCATTTCG	6960
CGGACAGCGG	CGCGCGGTGG	CCAATGACAC	CCGTATCTGG	CTCGGCGCGC	TAGACCAAAA	7020
CTTTTACCGC	AGCGCGGAAG	CCACCGACTC	CAAGCGCGCG	GCGCGGTTGG	GCTCGGACAT	7080
GGGTGAGTTG	TATATGCGCT	ACCGCGGCGC	CCCGATCAAC	CAGGAAACCG	TCTCGCTTGA	7140
CGGCAACCGG	GTGTCTGGA	GCGGCTCGTA	TTAGCAAGTC	AAGTTCAGCG	ATCGGAGTAA	7200
GCGCAACCGC	CAGATCTGGA	CGGCGTAAT	CGGCTCGCGC	GCGGCGAAGC	CACCGGACGC	7260
CGGCGCGCGT	CAGCGCTGGT	TTGTGGTATG	GCTCGGAGCC	GCCAACAACC	CGGTGGACAA	7320
GCGCGCGCGC	AAGGCGCTGG	CCGAATCGAT	CGCGCGTTTG	GTGCGCGCGC	CGCGGCGCGC	7380
GGCACCGCGT	GCTGAGAGCG	CGGCTCGCGC	GCGCGCGCGC	GCGCGGGAAG	TGCTGCTTAC	7440
CGCGAGCGCA	CGGACAGCGC	AGCGGACCTT	ACCGGCTTGA	GAATTCTGCA	GATATCCATC	7500
AACTGCGCGG	CGGCTCGAGC	ACCACGACCA	CCACCACTGA	GATCGGCGTG	CTAACAAAGC	7560
CGGAAGGGA	GCTGAGTTGG	CTGCTGCCAC	CGCTGAGCGA	TAAGTAGCAT	AACCGCTTGG	7620
GCCTCTTAAA	CGGCTCTTGA	GCGTTTTTTT	GCTGAAAGGA	GGAATATAT	CGGAT	7676



## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Gly His His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1             5             10             15

Pro Thr Ser Trp Gln Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
 20             25             30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35             40             45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50             55             60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65             70             75             80

Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85             90             95

Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100             105             110

Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
115             120             125

Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130             135             140

Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145             150             155             160

Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165             170             175

Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
180             185             190

Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
195             200             205

Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
210             215             220

Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225             230             235             240

```

Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly  
 245 250 255  
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val  
 260 265 270  
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys  
 275 280 285  
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp  
 290 295 300  
 Glu Ala Ser Glu Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser  
 305 310 315 320  
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala  
 325 330 335  
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp  
 340 345 350  
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile  
 355 360 365  
 Val Asn Asn Arg Glu Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala  
 370 375 380  
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp  
 385 390 395 400  
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp  
 405 410 415  
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala  
 420 425 430  
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu  
 435 440 445  
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly  
 450 455 460  
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg  
 465 470 475 480  
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser  
 485 490 495  
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu  
 500 505 510  
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala  
 515 520 525

Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro  
 530 535 540  
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro  
 545 550 555 560  
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro  
 565 570 575  
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn  
 580 585 590  
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser  
 595 600 605  
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr  
 610 615 620  
 Gly Asp Pro Pro Phe Pro Gly Glu Pro Pro Pro Val Ala Asn Asp Thr  
 625 630 635 640  
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu  
 645 650 655  
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu  
 660 665 670  
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser  
 675 680 685  
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys  
 690 695 700  
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile  
 705 710 715 720  
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp  
 725 730 735  
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

GTGGCGGCGC TCGCGCGCGC CAGCAGAGCG ATGTGCATCC GTTCGCGAAC CTGATCCCGG    60
TCGACGATGA GCGCGCGGAA CCGCGCGAGC ACGAGAAGCG TCAGGAAGCC GTCCACGAGC    120
GCGGTCCGCG CGGTGACGAA GCTGACCGCG TCACGATCA GCAGCACCCC GCGCATGGCG    180
CGACCAATG TCGACGCGT GATCGCGCGC ACGATCCGCA CCACGAGCGC CACCAGGAGC    240
ACACCGACGA GCGCGCGCGT GACCGCGGAG CCGATCCGCT TGTGACCGAA GATGCGCTCC    300
CGATCGCGCA TCAGCTGCGT ACCGACCGCG GGTGAACCA CCAGGCGGTA CCGCGCGTTC    360
TCTTCCACCG CATGGTTGTT CAGCACCTGC CAGCGCTGGC GGTGCGTAAT GCTTCTCGTC    420
GAAGATGGGG GTGCGCGCAT CCGTCACCGA GCGC

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## (2) INFORMATION FOR SEQ ID NO:211:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

TCGAGAAGTA CCGCGGATCC TCGTGGCGG ACGCGGAAGG GATTCGCGCG GTCGCGGAGC    60
GCATCGTCCG CACCAAGGAG CAGGCGATG ACGTGGTGGT CGTCGTCTCT GCCATGCGGG    120
ATACCGACCA CGACCTGCTG GATCTGGCTC AGCAGGTGTG CCGGGCGCGG CCGGCTCGGG    180
AGCTGGACAT GCTGCTTACC GCGGTGAAC GCATCTCGAA TCGGTTGGTG GCCATGGCCA    240
TCGAGTCCGT CCGCGCGCAT GCGGCTGCT TCACCGGTTG GCAGGCGCGG GTGATCAGCA    300
CCGCGACCCA CCGCAACGCT AAGATCATCG AGTTCACGCG GCGGCGGCTG CAAACCGCTC    360
TTGAGGAAAG CCGGCTGCTC TTGGTGGCGG GATTCCAAGG GGTGAGCCAG GACACCAAGG    420
ATGTCACGAC GTTGGGCGCG GCGGCTCGG ACACCAACCG CGTCGCGATG

```

## (2) INFORMATION FOR SEQ ID NO:212:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

GGCGCGCGTA CCGGCGCGG ACAAACAAGG ATCGATTGAT ATCGATGAGA GACCGAGGAA    60
TCGTGGCGCT TCCCGAGTTC ACCGACGAGC AGCGCGCGCG CGCGTTGGAG AAGGTCGCTC    120
CGCACCTCG AGCGCGAGCA GAGCTGAGG ATCGGCTCAA GGTGCGCGGC ACCAAGCTCA    180

```

CCCAGGTCCT	CAAGGACGCG	GAGAGCGATG	AAGTCTTGGG	CAAAATGAAG	GTGTCTGCGC	249
TGCTTGAGGC	CTTGCCAAAG	GTGGGCAAGG	TCCAGGCGC			279

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACACCGTCGA	ACTCGACGAG	CCCCCTCTGG	AGGTGTGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGGCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACCGTCGA	120
GGTCGGCGGC	GAGGTGTCTG	TCATTGGCGA	CGCCCATGAT	GCCGCGGAGG	CCCGCGGTCC	180
GCCACCGCCG	AAAGTCTCTG	CCGCGCCCAAC	CCGAATCCA			219

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TGCTGTCGGA	CATCGGCGCC	GCGCGCGGCT	CGAGCGGCGC	ACCGAAGGCG	GTCCCCGAGC	60
CAGCGCGGAC	GCGGAAGGCG	GAACCGGCAC	CATCGGCGCC	GCGCGGCGCG	CCAGCGCGTG	120
CGCGCGAGCG	CGCACCGTAC	GTGACGCGCC	TGGTGCAGAA	GCTGGCGCTC	GAAGACAACA	180
TGGACCTCGC	CGGGGTGACC	GGCACCGGAG	TGGGTGCTCG	CATCGGCGAA	CAGGATGTGC	240
TGGCGCGGCG	TGAACAAAAG	AAGCGCGCGA	AAGCACTGCG	GCGCGCGGCG	CAGGCGCGCG	300
CGCGCGCGCG	CGCGAAAGCG	CGGCTGGAAG	ATCGATGCGC	GC		342

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGGTCTTGGT	CAGTATCAGC	GCGGACGAGG	ACGCGACCGT	GCCCGTGGCG	GCGGAGTTGG	60
CCCGGATCGG	TGTGGCTGCC	GACATCGGCG	CCGCGCGCGC	CCCGAAGCGC	GCAACCGAGC	120
CGGTCCCGGA	GCCAGCGCGG	ACGCGGAGG	CCGAACCGCG	ACCATCGCGG	CCCGCGCGCG	180
ACCGAGCGCG	TGCGCGCGAG	GCGCGACCGT	ACGTGACCGC	GCTGGTGGGA	AAGCTGCGCT	240

CGGAAAACAA	CATCGACCTC	GCCGGGGTGA	CCGGCACCTG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGGCGCGC	GCTGAACAAA	AGAAGCGGGC	GAAAGCACCG	GCCCCCTGAG	360
CGCTTCATCA	CCCGGTTAAC	CAGCTTGCCC	CAGAAGCCCG	CTTCGACCTC	TTCCCGGGTC	420
TTGGTCCGCT	GCAGGCGGTC	GCGGAGCCAG	TTGAGGTTAG	GCUGCCGAAA	TCTTCGAGTT	480
CCCCAGGAAG	GGCACCCGGA	ACAGGGTCCG	CACCC			515

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CGGACCCCAA	GCTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCCGACC	CACCAAGCCG	60
TGACTCAACA	GGCGCCGCAA	GTHATCCGTA	ACCAGCCTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGCG	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGGCGG	180
ACCAGGCCGC	CGCCGCCGGA	GACGTTGCCA	AGGCCACCGA	ATACAACAAC	GCCCCCGAGG	240
CGTTCCGAGC	CCAGCTGGTG	ACCGCCGAGC	AGAGCGTCGA	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCCCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCCGT	CGAACGAAAT	GCGATGGTGC	360
TCCAGCGAGG	GATCGCCGAG	CGAACCAAGC	TGCTCAGCCA	GCTCGAGCAG	GCGAAGATGC	420
AGGAGCGAGT	CAGCCGATCG	TTGCGGTGCA	TGAGTGAGCT	CGCCGCGCCA	GGCAACACGC	480
CGAGCCTCGA	CGAGGTGCGC	GACAAGATCG	AGCGTCGCTA	CGCCAAAGCG	ATCGGTTCCG	540
CTGAACCTTC	CGACAGT					557

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CAGGATAGGT	TTGACATCT	ACCTGGGTTT	CGCACCCGGT	GCGCGACCTT	GTGATAGGCC	60
AGAGGTGGAC	CTGCGCCGAC	CGACCATCGA	TGAGGAGTTC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTCGGT	GAGAGCCTCA	CCGAGGCGAC	GCTTACCCGC	TGGCTCAAAC	180
AGGAAGGCCA	CACGGTCGAA	CTCGACGAGC	CCCTCCTTGA	GGT		223

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

AAGAAGTACA	TCTGCCGCTC	GATGTCGGCG	AACCACGGCA	CCCAACGGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAACC	CCAGTCCCGG	CGCACAACCA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CCGCCAGCCA	CCACATCCCG	GGCGTSCCGA	CCASCATCTC	GGCCTTGACG	180
CACGACTGTC	CGCCCGAGCC	TGCAACGTCT	TGCTGGTCSA	TGGCGTACAG	CACCGGCCCG	240
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GCTAGTTGCC	TGCGGAATTC	300
GTCAGCCCCG	CGTGGAAAGT	GAACGCTTTG	GGGTGTATTT	GCCAGAGCGA	GCGCACGGCG	360
TGGGCGACCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCCCGAA	CGCGATCAAC	480
CCGACCGCAT	ACCGCTGGG	AAGCACCTCA	CGCCGCACTG	TTCCGAGCCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTCCGCG	CGCCACGTCA	ACGCCAGC			578

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCAGCG	CGCGGCCCGG	TTGGAGAAGG	CTGCTGCCGC	ACGTGAGCGG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GGTCTCTAAG	GACCGCGAGA	180
GCGATGAAGT	CTTGGGCAAA	ATGAAGGTGT	CTGCGCTGCT	TGAGGCCCTG	CCAAAGGTGG	240
GCAAGGTCAA	GGGCGAGGAG	ATCATGACCG	AGCTGGAAT	TGCGCCCGAC	CCCGCCGCGT	300
TGCTGGCCCT	GGTGACCTTC	AGCGCAAGCG	CGTGTGGA	AAGTTGGGCT	CCGCTTAACC	360
CGCGCGCGCG	ACGATGCGCG	CGGGAAGGCG	TGTGTGCGCG	GTACCCCGCG	ATACCGGCGA	420
GAAGCGCGCT	GACAGGCGCA	GCTACCAATT	CAGCGCGAAC	CGCCCGGTGG	GGGGGAACCC	480
GCCC						484

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AGGACTGGCA	CGGCCAGCCA	CCACATCCCG	GGCGTSCCGA	CCAGCATCTC	GGCCTTGACG	60
CACGACTGTC	CGCCCGAGCC	TGCAACGTCT	TGCTGGTCSA	TGGCGTACAG	CACCGGCCCG	120
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GCTAGTTGCC	TGCGGAATTC	180
GTCAGCCCCG	CGTGGAAAGT	GAACGCTTTG	GGGTGTATTT	GCCAGAGCGA	GCGCACGGCG	240
TGGGCGACCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCCCGAA	CGCGATCAAC	360
CCGACCGCAT	ACCGCTGGG	AAGCACCTCA	CGCCGCACTG	TTCCGAGCCA	CGGTCTTTGC	420

ACTTGGTACT GAGTCCGCG CCCACGTCG AACGCCAGCG CCATCCGCGC GAAGACAGC 480  
ACGAAGTACA CGCGGACCA CTTGGTGGCG CAGGCCAATC CCAAGCAGCA CCCCAGC 517

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn  
1 5 10 15  
Leu His Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu  
20 25 30  
Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp  
35 40 45  
Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg  
50 55 60  
Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His  
65 70 75 80  
Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Gln  
85 90 95  
Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn  
100 105 110  
His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His  
115 120 125  
Leu Pro Gly Leu Ala Val Arg  
130 135

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg  
1 5 10 15  
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val  
20 25 30  
Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu  
35 40 45  
Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu  
50 55 60  
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile



```

65          70          75          80
Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
      85          90          95
Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
      100          105          110
Pro Gly Arg Leu Gln Thr Ala Leu Gln Glu Gly Arg Val Val Leu Val
      115          120          125
Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
      130          135          140
Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
145          150          155

```

## (2) INFORMATION FOR SEQ ID NO:223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
1          5          10          15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
      20          25          30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
      35          40          45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
      50          55          60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
      65          70          75          80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
      85          90

```

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
1          5          10          15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
      20          25          30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
      35          40          45

```

Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys  
 30 35 60  
 Val Ser Ala Gly Pro Thr Arg Ile  
 65 70

## (2) INFORMATION FOR SEQ ID NO:225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro  
 1 5 10 15  
 Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro  
 20 25 30  
 Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr  
 35 40 45  
 Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly  
 50 55 60  
 Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu  
 65 70 75 80  
 Ala Ala Ala Gln Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala  
 85 90 95  
 Gln Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Gln Asp Pro Met  
 100 105 110  
 Pro

## (2) INFORMATION FOR SEQ ID NO:226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly  
 1 5 10 15  
 Gly Glu Leu Ala Arg Ile Gly Val Ala Asp Ile Gly Ala Ala Pro  
 20 25 30  
 Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro  
 35 40 45  
 Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala  
 50 55 60  
 Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser

```

65              70              75              80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
      85              90              95
Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Ala Gln Gln Lys Lys Arg
      100              105              110
Ala Lys Ala Pro Ala Pro
      115

```

## (2) INFORMATION FOR SEQ ID NO:227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
1              5              10              15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
      20              25              30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
      35              40              45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
      50              55              60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
65              70              75              80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
      85              90              95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Ala Gln Ala Lys Lys Ala
      100              105              110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
      115              120              125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Gln Gln Val Ser
      130              135              140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145              150              155              160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
      165              170              175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
      180              185

```

## (2) INFORMATION FOR SEQ ID NO:228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Glu Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
          20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
          35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
          50           55           60
Leu Asp Glu Pro Leu Val Glu
          65           70

```

## (2) INFORMATION FOR SEQ ID NO:229:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
          20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
          35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
          50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
          65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
          85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
          100          105          110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
          115          120          125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
          130          135          140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
          145          150          155          160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
          165          170          175
Arg Ser Leu His Leu Val
          180

```

## (2) INFORMATION FOR SEQ ID NO:230:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Ala Leu Glu Lys Ala Ala Ala
 20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
 35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
 50           55           60
Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65           70           75           80
Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85           90           95
Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
100          105          110
Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
115          120          125
Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
130          135          140
Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
145          150          155          160

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1           5           10           15
Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
 20           25           30
Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35           40           45
Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50           55           60
Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65           70           75           80
Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85           90           95
Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
100          105          110
Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His

```

```

      115              120              125
Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
      130              135              140
Ser Arg Arg His Val Gln Arg Gln Arg His Arg Ala Glu Gln Gln His
      145              150              155              160
Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
      165              170              175
Pro Arg

```

## (2) INFORMATION FOR SEQ ID NO:232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

ATGCCAAGCC GGTGCTGATC CCGAGCTCC GCGAATCGGT GACCGAGGGC ACCGTCATTC      60
GTTCGCTGAA GAAGATCCGG GATTCGGTTC AGCTTGACGA GCACTCGTG GAGGTGTCCA      120
CCGACAAGGT GGACACCGAG ATCCCGTCCC CGTGGCTGG GGTCTTGTC AGTATCAGCG      180
CCGACGAGCA CCGCAGGTC CCGGTGGGG CCGAATTGGC CCGGATCGGT GTCGCTGCCC      240
AGATCGGGCC CCGCGCCGCC CCCAAGCCCC C

```

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Ala Lys Pro Val Leu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly
  1              5              10              15
Thr Val Ile Arg Trp Leu Lys Lys Ile Gly Asp Ser Val Gln Val Asp
  20              25              30
Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro
  35              40              45
Ser Pro Val Ala Gly Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala
  50              55              60
Thr Val Pro Val Gly Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Glu
  65              70              75              80
Ile Gly Ala Ala Pro Ala Pro Lys Pro
      85

```

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```
GAGGTAGGCG ATGCCCGGAG GAGCACCCCA GGACCCCGCC CGAACCGCGG GTGCCCGTCA    60
TCGATATGTG GGCACCGTTC GTTCCCTCCG CCGAGGTCAT TGACGAT                      107
```

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```
ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GCGCTTGTG    60
TTTCTTGCTT CGTTTCCGAG CCGAGATCCA CTTGACCCGC ATCAGCCCGA CATGACGAAA    120
GGCTATTGCC CCGGTGGCGG ATGGGGTTTT GCGCACTTGG CCGTGTGCGA CCGCGAGAAG    180
TACCGCGACG GCTCGTTTTG GCACCACTGG ATGCAACCGT GGTTTACCGG CCCACASTTT    240
TACTTCGATT GTGTCAGCGG CCGTGAGCCC CTCCCCGGCC CCGCGCCACC GCGTGGTTGC    300
GCTGGCGCAA TTCCCTCCGA GCAGCCCAAC GCTCCCTGA                      339
```

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```
Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1           5           10           15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 20           25           30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35           40           45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50           55           60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65           70           75           80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
```

Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro  
100 105 110

## (2) INFORMATION FOR SEQ ID NO: 217:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (22) MOLECULE TYPE: GINA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 237.

GTGACACAGG	TGGGCGGCGC	ACCAACCGCG	GCAGCGGCGC	CGGCGGCGCG	GCGGCGGCGT	66
CGGCGGCGCA	CGGTGCGCGC	GGGGGTAAAC	CCACCGGCTC	AGGCGGCGAG	GGCGGCGCGG	120
GTGGCAATGG	CGGTGATGGG	AGCTTCGGCG	GTACCAAGCG	CCCGCGCTTC	ATCGGGGTCA	180
CGGGCGCGCG	CGGCGCGCAC	GGCGGCAAGG	GCGGCGCGCG	TGGCAGCAAC	CCCAACCGCT	240
CAGGTGGCGA	CGGCGGCAAA	GGCGGCAAGC	GCGGTGCGCG	CGGCAACGGG	GGGTGATCGG	300
GCGGCAACAG	CGGCATCGTC	GCGGTTGCGG	GTGGGGCGCG	TGGCGCTGCG	GGCGCGCGCG	360
GAAACGGCAG	C					372

## (2) INFORMATION FOR SEQ ID NO. 148:

## (1) SEQUENCE CHARACTERISTICS:

- (7) LENGTH: 424 bases  
(8) TYPE: nucleic acid  
(9) STRANDEDNESS: single  
(10) TOPOLOGY: linear

(U) ~~SECRET~~ ~~NOFORN~~ ~~CONF~~

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:238.

GTCTGGGTTCC	CAGCAACCGCG	CCGGGCGCGCC	CCTAGCGCGCC	GGGCGGACCA	GCCCCCTTTC	60
TGAGCTTCOTT	CAAGAAAAGG	GGCTTCTCTT	TGGTCGGGCA	TGTTGGCATG	ATCGTGAGCC	120
ATGGGCAACA	TGCACTGCA	CATCTCGCG	AAGGTCTAGC	TCCATGCGA	TGCCCCGCGC	180
GGTGGTGAAC	ATCGGTCTAG	GGTCTATAGC	AGGGTTGCG	GTACCTGTTT	CCGACGCACA	240
GGGTTGGAG	CCCGGGGTTG	TGTCTACGC	GGTCTCGGA	AAGGGTCTCG	TGGGCAACAT	300
CGTGGGCGC	CCAAATGGGT	GGGAGCGGT	GTTCACCAAG	CGTTCCAGG	CGTTTTGGGT	360
CGAATTACCG	GGTGCACA	ACTGGGTGA	CATCGGGCTG	CCCGAGGTGT	ACGACCATCC	420
CGAC						424

## (2) INFORMATION FOR SEC ID NO. 240.

## (1) SEQUENCE CHARACTERIZATION.

- (A) LENGTH: 117 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (10) MOLECULE TYPE: COM



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GCGATGGGGG	CGCGGGGTAC	CACCGCCAAT	GTGGAACGGT	TTCCCAACCC	CAACGATCCT	60
TTGCATCTGG	CGTCAATTGA	CTTCAGCCCG	GCGGATTTGG	TCACCGAGGG	CCACCGTCTA	120
AGGGCGGATG	CGATCCTACT	CGCGCTTACC	GACCGGCTGG	CTTTCGCGGA	GCGCGCGGAT	180
TGGGACTTGG	TGGACTGCGA	GTTGCGGACG	ACCGTCACCG	CGGACACGGT	GCGCATCGAC	240
GTGATCGCGG	ACGATATGCG	TCCCGAAGTG	GCGGCGGGCT	CCAAACTCAC	CGAATCGCTG	300
CGGCTCTACG	ATTGCTC					317

## (2) INFORMATION FOR SEQ ID NO:240:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGGGCTATGC	GCTTCGCGAG	CGGTGCGCGG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCAGG	ATCGCACTGT	GCGGTGCTGC	ACCGACACCG	CGCTCCCAAG	120
TGAAGTCAGG	GCGGAAAATC	GCGGAAAATC	TCCGCTTCAG	TTCAGGCTCG	GCGGCTAAGC	180
GTTCTGGAAG	TTGGGTGCGG	GCTTCTCGGC	GAACGCGCGC	GCGGCTTCTT	TGGCGTCTTC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTGATCTTGG	AACGCTCTCT	TTTCGGGCTT	300
GCACTCGGTC	TCCCGGATGG	ACCGCAAGAT	GCGTTCACCG	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGCTG	GCAAGTTCTA	GAACCTTGGT	CAACGCTCTG	CGTTCGGGCA	CAGGTGGCGG	420
AT						422

## (2) INFORMATION FOR SEQ ID NO:241:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GCGTCCGCTT	GAACACCAAG	CGCGGCTTGC	CAGATCTGCC	GGACTCGGTA	GTGCGGCGCG	60
TGGGCTCTCT	GCTCTCTGGA	CGCGGCGCGG	CGACCATAGG	GTGCTTAATG	CCGAGGTAGC	120
GCGCCAGGTC	CATCGAGTGG	ATGATGATGC	GACTCTCCAG	CTGCGCGAGC	GCGAGCTTGG	180
CATCGGCGCT	GATCAGCCAG	GACGCTTAGG	ACAAAGTCGAT	CGAATGCATA	GTGGCTTCCA	240
GAGTGGCGCT	GCGACTTCCG	GCGTCTTCCA	CGGCAATGTC	CTTGATTTCT	AGCTCCGCTT	300
AGTCTTCCCG	CATCGGCTTC	GCGATGAATG	GGACCGCGAG	GATGCGGACA	AACGCTCTTC	360
ACCTCAGGTT	TGCGGCTTTC	CGCAGAGTGG	TGACAGCGCG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

## (2) INFORMATION FOR SEQ ID NO:242:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

AGACCGGCGA	GGGTGTGCTC	GTCGCCCCCG	GCATTGTGCA	TAATCTGCSC	TGGGTGAGC	50
CGCCGATCRA	CTAGTGAGGC	GCAACGCTAG	GCTTTGGGAT	ACCCACAGCT	AAAAAGTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTCGCGC	CTACGCGCGC	ATGTGCGCGA	180
CCGAACCCCT	GACCAAGACC	ACCATCAGCC	GTGCGGACCC	GGGCGCGCAC	GACATGCGCA	240
TGGACATCAA	ATTGCGCGCA	ATCTGTGCTT	CGGACATCCA	TACCGTCCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACCTGTC	GTGCGTTC				327

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Asp	His	Gly	Gly	Pro	Ala	Thr	Asn	Pro	Gly	Ser	Gly	Ser	Arg	Gly	Gly	1	5	10	15
Ala	Gly	Gly	Ser	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Ala	Thr	Gly	20	25	30	35
Ser	Gly	Gly	Lys	Gly	Gly	Ala	Gly	Gly	Asn	Gly	Gly	Asp	Gly	Ser	Phe	40	45	50	55
Gly	Ala	Thr	Ser	Gly	Pro	Ala	Ser	Ile	Gly	Val	Thr	Gly	Ala	Pro	Gly	60	65	70	75
Gly	Asn	Gly	Gly	Lys	Gly	Ala	Gly	Gly	Ser	Asn	Pro	Asn	Gly	Ser		80	85	90	95
Gly	Gly	Asp	Gly	Gly	Lys	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Gly	100	105	110	115
Gly	Ser	Ile	Gly	Ala	Asn	Ser	Gly	Ile	Val	Gly	Gly	Ser	Gly	Gly	Ala	120	125	130	135
Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Asn	Gly	Ser						140	145	150	155

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
1      5      10      15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
20      25      30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
35      40      45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
50      55      60
Ser Glu Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
65      70      75      80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ala Ser Lys Leu Thr
85      90      95
Glu Ser Leu Arg Leu Tyr Asp Ser
100

```

## (2) INFORMATION FOR SEQ ID NO:245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
1      5      10      15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
20      25      30
Ala Pro Thr Pro Pro Ser Asn Val Asn
35      40

```

## (2) INFORMATION FOR SEQ ID NO:246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
1      5      10      15
Val Pro Pro Val Ala Ser Leu Leu Ser
20      25

```

## (2) INFORMATION FOR SEQ ID NO:247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1             5             10             15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
 20             25             30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
 35             40             45
Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

GCTTGGAGCC CTGGAGCCGAC GGTGTGGGTC TGGGGGTGCA TTCGTTCTCG GCGAAGTCA 60
ACTAAGGACC AGTTTGACAC CCAACCGGCG GCCCGGCATG GGGCGTCGCG GCGTAGAAGC 120
TTTGACCGCG GCGCGAAGAC TTGCTGCTG CGGCCCATGC AGATCGCACA GCGTTGCTTG 180
AACATCGGGT GAGCGCGGTC GTACGCGCAG GCT 213

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

CCGAGCTGCT GTTGGGCGCC GCGGTGCGCG GCGGCGCGCG TGGGGCGCGC ACCGACGGCG 60
GGCGCGGTGC TACCGGCGCG ACCGCGCGAC ACCGCGGAGT CCGCGCGGAC GCGCGATGGC 120
TGGCAGCGCG CGCGGCGCGC GCGGCGCGCG GCGAAGCGCG GCGAGGTGAT GCGCGAGCG 180
ATGCTGCGCG GTTGGGTGAT ACCGCGCGCA CGGCGCGTAC CCGCGCGCGC GGTGGCGCGC 240
GCGGTGCGCG CCACTGCTG CTGGCGCTG GCGGACAGCG CGGCTCGCG GCGCGCGCGC 300
GACAAGCGCG CACCGCGCGG GCGCGCGCGA GATGCGGTTC TGGGGGTGT CAGTGGCACT 360
GGTGGTA 367

```

## (2) INFORMATION FOR SEQ ID NO:250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

AAGGCCTGAT TGGCAAGGCG ACCGCGCAGC GCGCCGTAGC CCGCGGACCG CCCAGGCCCC    60
GACCGCAGCG GCGCGTGTCT GACCGGGTCA GCGACCAAGC GCGCTGACCG TCGCGCTGGT    120
CTACTTCGAC GCGAGCGGCT TCGTCAAACT TGTCAACACC GAGACAGGGA GCTCGCTGGC    180
GTCCGCTGTA TGGGACGGCT GCGACGCGCG ATTGTCCGAC CGCCTGCGCT ACCCGGAAGT    240
CGCGCGCGGA CTGCGTGCAG CCGCGCGCAA TCACGACCTA ACCGAATCCG AGCTCGCGGA    300
CGCGGAGGCT GACTGGGAGG ACTTCTGGGC CGCACCGCGC CAGTCGAACT CACCGCGAGC    360
GTTGAACAGC ACSCCGGCA CTTGCGCGCA ACACATGCTT TACCGCGAGC CGACACGCTT    420

```

## (2) INFORMATION FOR SEQ ID NO:251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

CTCTTGTGCG TGGCATCGCG GGTACCGGCG GAACCGCGCG CAACCGCGCT ATGCTGCGCG    60
GCGCGCGCGG GCGCGCGGCT GCGCGCGGGT TCAGCTTCAG CACTGCTGCT GCGGCTGCGG    120
GCGCGCGCGG GCGCGGTGCG CTGTTCAACA CCGCGCGGTGT CCGCGCGCGG GGTGCGCGAG    180
GTACACAGCG CCGCGCGGCG GCGCGCGCGG GCGCGCGCGG GTTGTGTTGT GCGCGCGCGA    240
TGGCGCGCGG GCGCGGATTC GCGGATCAG GAACGCTCGG CACCGCGCGG GCGCGCGG    300

```

## (2) INFORMATION FOR SEQ ID NO:252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
1           5           10           15
Ala Lys Val Asn
20

```

## (3) INFORMATION FOR SEQ ID NO:253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1             5             10             15
Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly
 20             25             30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
 35             40             45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
 50             55             60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
 65             70             75             80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
 85             90             95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
100             105             110
Ser Gly Gly Cys Gln Trp His Trp Trp
115             120

```

## (2) INFORMATION FOR SEQ ID NO:254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1             5             10             15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20             25             30
Arg Arg

```

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1           5           10           15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
 20           25           30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
 35           40           45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50           55           60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65           70           75           80
Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85           90           95
Ala Gly Gly

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

TCTGTCTCCG CGCCGCGCGG GTGGGCGGTG TTGGCGGTGA CGGTGTGGCA TTCTGGGCA 60
CGGCGCGCGG CGGCGCGCGT GTGGCGCGG GGGCGGCTGG GCTGTTCAGC GTGCGTGGCG 120
CGGCGCGCGC CGGCGGAATC GATTTGGTCC GGAACAGCGG TCCCGGCGGG TCCGCGCGGT 180
CGGCGCTGCT CTGGGCGGAC GCGGTGCGG CGGCGCGCGG TGGGGTCCGG TCCACTACCG 240
CGGGTGCGCG CGGCGCGCGC GGCAACGCGA CCTGTGCT AA 282

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

CGGCACGAGC CTTCTACTCG GTCAACTGAT GCGCTGATCG TGACCTTCGG GCGCGCGGAT 60
CAGTCTTTCT CAGGACCGAC GTAATATTCC AAAACCAATC CGCGCGCGCA GCGGAGGATG 120
AATGCCACAC CGCGCGCGAT CAGCCACCGG AGCLACACG CGATGCGGAC GCGTGGCACC 180
GAGCGCGACA ACCCGACCAT GATCGCGCAC CAGCTATCGG GACTGAAGAA TCCAGTTCT 240
CGTGGCGCGT CGCTGATTTC AGCGCGTTCC TAGTCTCGG GCGCGGAATC TAACCGGCGG 300
GCCACAAACC GGAAGAAGTT GCGGACGATC AACCGCATGC CCGCGGTGAG CGCLACGCA 360

```

ATGGTGCCAG CCCACTGAC ACCACGGGTG GCGAACATCG AGTCAACAC GCGGT

415

(2) INFORMATION FOR SEQ ID NO:258:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TCACCGCGTGG AACGGTTCCT AACACTGATA CCTATGCTTG TCAGCGAGCA GATCAAGTCC	60
AGTCCGACCA ATGCCAGCAG ATCATCGGCT AGGCTCAGCG TTTCGCTTGG GACGAGACGG	120
TATGAGTTC TGGCGTTGCA CGTCCGTTGG CTTGGTGGGA AGTCTGACCC GGCATCAGAA	180
CGGTTGTCAA TACCACTCTT TGGGGGATAT GGCCTATTTC GTGTCTCTCG GCGGCTCCAC	240
CGGATCCCTT TTGGAAGCTT GCGCAAGCTC GGTCCAGTTA CCGGCTGTTT ACTGCGCGCT	300
GGCGTAGCTG CCGGCGCTCG ATCGGTTTCA ACCTCATCGC AATCCCGCCA ATGGGTGAGT	360
ACCTGACGCT CCT	373

(2) INFORMATION FOR SEQ ID NO:259:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCAAACCGGA CAGGCGGCA GCGACCGTCC GAAGTTGAC CACCGTCCGC CTTCCATGTA	60
GCCACCGGT GACGACGGCG TAGACAGCAG ATCCGTGGAT CCGCGCTTCC GTGTCTCTCC	120
GGCGGAGTAC CCGCGGCGCG AACCGGCGG ACCAAAGCAA CCGCATCGAT ACCGGGATCG	180
CTACTCGTCC CCAATTCCAG CTCCGTCCAC AAGCTTGGCG CCGCACTGCA ACCCGGCTGA	240
ATGATTGAGT TTAACCGCT TAGCAATAAC TAGCATAACC CTTTGGGCCC TCTAAACCGG	300
TCTTGAGGGG TTTTCTGCTG AAGGAGGAA CTATATCCGG ATAACCTGCC GTAGTAGCGA	360
AGAGGCGGCG ACCGATCGCC GTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGACGGG	420
CCC	423

(2) INFORMATION FOR SEQ ID NO:260:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:260:



AGTGGCCAGC	CGGTCCGCCA	ATGCATCCAG	CTCCCGGTAC	GTCAGCTGAC	CATCCGCCCA	60
ACTGACCCGC	ACCGACTCAG	GCTGTGCCGC	AGCGATTTCG	GCGAACCSCG	TATGCCACCG	120
GGGTGCCGAC	GTCSTCAGAT	CCGGCAGGCG	GGGTCCGCTC	GGATCGTGCT	CGCCCTCCAG	180
CAGAATGTGG	ACGTCCGCCA	GCGGCCGATC	CCACCGGCTG	ACCAAGCGCT	GTAACACAGC	240
CACCAACCCG	CTGCCGAGGC	TTTCGGGCCG	CATCGTGCCC	AGCGCACCTT	CGAGCACCTG	300
CACAGCAGCG	GTGAGCTCAC	CGGTGCTGCG	GTCCGCGCGG	ACGGTCACCG	GAAAGTGCCA	360
CAAACTCTCT	AGCCCCACCG	GACCGAAGCT	CACCCCGTTT	GCRA		404

## (2) INFORMATION FOR SEQ ID NO:261:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GTCCCTGCTG	CAGGCTGCTT	TTCCGAACCG	CTGGCTAACT	TGGCACCCCG	GTATCCGCCG	60
ACCATCGAAG	CCGCCCAACC	GGCGGTGTCA	CCGCTACTT	CCCAAGACCC	GGCCCGTGCA	120
GTCCGACCA	TGAGCGGCCA	CCCCCGGCG	GCACTATTG	ACAACGGCAC	CGCCCAATTG	180
GTGCTCTG	GGCCCGGCC	CGATTCCGCG	GCACCGGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACCTTG	CACCGCGCTT	CATTTTCTG	CGCGGCCCGG	CAGCCCGCTT	GACCAGCGAC	300
GACCAACGCA	CGGCTTCTT	TGCCCGCCCG	GGCGGTACT	TCTGGGCCA	CCTGTCTCTT	360
GGTCACACCG	CACGAGTGAA	TGTGCTTGAC	GCAGCGCACA	CGGATTTTAC	CGCGATCCCG	420
C						421

## (2) INFORMATION FOR SEQ ID NO:262:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:262:

ATGCATATCA	CGCTCAACCG	CATCTTGGCT	GGATCTTTG	GGGCGCGCGG	CAGTGAACTA	60
GACGAGCTGC	GGCGCTTCAT	TCCGCGGTGG	GTCAGCGTGG	GCTCGCGCTT	GGCGCGCGCTA	120
CGGAAACCCA	AACGCGACTA	TGGCGGCTT	AGCGCGTGGG	GGCGCGTGGC	CGAGTGCGCG	180
CGCCAGTACG	ACACTGTTCAT	CGACGAGCTC	ATCGAAGCGG	AGCGCGCGCG	CCCGAACTTC	240
GGCGATCCGA	CGGAGTTTTT	GGCTTTCATG	CTGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTGCGCGA	AGGACATTGG	CGACGAACTG	CTCACGCTGC	TTGCGCGCGG	GCACGAAACC	360
ACGCGCGCGG	CATGGGCTGG	GCCTTCGAAC	GGCTCAACCG	GCACCGCGAC	GTGCTCGCGG	420
CTCTGG						426

## (2) INFORMATION FOR SEQ ID NO:263:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GTCTCTGTCG	CAGGCTGTTT	TTGGAACCCG	CTGGCTAAGT	TGGCAGCCCG	GTATCGGCCC	60
ACCATCGAAC	CCGCGCAACT	GGCGGTGTCA	CGGTTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCC	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	CCCCCGGGCG	CGATTGGGCG	GCACCGGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCCG	CAGCGCGGTT	GACCAGCGAC	300
GACCAAGGCA	CGGCTTCTT	TGCGGCGGCG	GGCGGCTACT	TGGTGGCGCA	CCTGTCTCTC	360
GGTCACACCG	CACGAGTGA	TGTGGCTGAC	GCACGCGACA	CGGATTTTAC	CGCGATCGCC	420
CGCGGCTCGG	ACGCGAAGCT	GGTGGTGGCG	AGCGGAGATG	GGCGGCTCTA	CACGCTTGGC	480
AAGAACCCCG	AGTTGACCG	CTGGGCGCGC	GCCACCGTAG	CC		522

(2) INFORMATION FOR SEQ ID NO:264:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 739 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GCTGGGGGCG	ACGCGGCTCG	GGCGGCGGCA	GGCGGCTGGG	CGAGACCCCG	CGCAAAACCA	60
ACCGGTGGCG	TTAGTGGCG	GGCGGCGGCG	CGGTGGTGGT	CGTGGTGGTG	TTGGGGCGCA	120
TGGGCTGGTG	GATCGGCTG	CGCGGCAAGC	CGGTACAGCG	GGTTCAGCG	GTTCGGGAGG	180
AGCGGCTTAC	CGCGTACTG	GTGAAGTCTT	CAGAGTCAAA	CGCGGCTGATG	GGTCTGTCTT	240
CGATGCAAGC	GGCGCAAGCG	ATGACATCGA	TGGACTCTTC	GGCGGTGACG	GTGTCTCTGC	300
CGGACTGGCA	GGCGGCGGCG	TATACGAGCG	AGGATCGCGT	GTATGCGGCG	ACCGGCTACA	360
CGCGGCTCAA	CGCGTGGATT	TGATCGGAGC	CGCGGCGACAA	CTACGAAACAT	TGGGTGAACC	420
AAGCGGCTCT	CGCGTTTGGG	ACCGGCGGCA	AAGCGCGGCG	GTTCGTGCGG	ACTTCGGGCG	480
ACAAATGGAA	GAAGTGGCG	GGCAAGACCG	TCACCGTCCAC	GAATAAGGCT	AAGACTTACT	540
GGTGGAGCTT	TGGGAGCTTC	AAAGGCAAGT	CGCGGAGGAT	CACGGTGATA	GACACCCAG	600
AAGCGGCTGA	GGGCTGGGAA	TGCGCAAGCG	CGATGAGCGT	GGCGAACAAT	GTGTTTGTCC	660
AGTCAAGCG	ATGCGGCTAC	CAGATCACCA	ATCAAGCAGG	CGGATCGCG	CGGAGATCT	720
GTGACAAAG	TCAACAGG					739

(2) INFORMATION FOR SEQ ID NO:265:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGACGTCGTC GAGGCCGCCA TCGCCCGCCG CCAAGCCGTT AACCCCGCAC TGAACGCGTT 60  
GGCGTATCC 69

(3) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

ACTGCACCCG SCAGGGGCGA CCAACCGATC GGTCACACTA GCACTGCCCG TGGAGGCCCG 60  
CCCCCGGTCT GTCCCTTCGG ACCGGGGAAC CTTCGGCAGC GCGGCTCCAG AAGCGTTGGA 120  
GGGAGAGTTC GACCAACCTA TCGACGAGCG GTTCGGCGTC TTCAGCTCCG CCACTCTCCG 180  
CCAAGCGCTG CCGGCTCCCG TCACCCCGAT GACGCTGGAT GTCCAGTTGA GTGCACTGCC 240  
GCGCGCGGCT CGGCGCATCG GTCCGCTACT GCGGCTTGGC GGTGTCCTTC CCGATGAGTC 300  
GGAGAGAAGA GCCATCGCGG TGTTCGGTCA CCGCCCGTAT ATCGGAGTGT CCGCCAATAT 360  
TGTGGCGCGC GCCCAACTGC CCGGCTGGGA CCGCGACGCC GTAACCCGCG GGGCACTCGG 420  
CGAGCAACCG CAGGTCACTG AGCTGCTTCC GTTGTGTGCA CCGCAACTTG CCGGCGGACC 480  
GCTCGGCTCG GTCCGCAAGG TGGTGTGAC GGCACGCTCG CTG 523

(3) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GTGTCTGTCT GTTCGGGTA GAGCGACTT CCGCGCGCGG CGCCGCGCGG GGAGCGCGCT 60  
CTGCAGGAAC CGTTCGCGCG GTTCGCGCGG GGGCGACCAA AGCCCGGATC GATTGCGCCA 120  
CGCGCTTGGC CGCGCGCTTG TCCACCGCGT TGTTCGCGGT CCGGAGCGAT ACCACAAACC 180  
AACCGTGAAG CGCGCTCGCG TCCGCTGCGT TCGCGCGCGG CGAC 224

(3) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TCACTGACT CCGCGCGTCC ATCGCGCGCG CGCGCTTCTC ATAGCTGCCG CGCGAGGCCA 60

```

TGAAGTGGCTC TTGGCCATAG CCGGCKTTTG TCTGCGCTTT GTCCAAACCC TCAGCGCGCC 120
CGTAGTGGCC TTGGTTGAGC CCGCAGTTAC GCGCGACCGG AATCCAGAGC CGATCGCGCC 180
TGTCCAAACG CAGATCGCGC GTGGTGTATC CCGCGCGCAG CAACGAGGTG TAGAGCACGT 240
CGGGCAATAG GTGGTGTTCG GCGATCAGCT CCGCGCTTCG AACCGCGCTG GCGTGGCGCT 300
TGTCCGTGAG GCGGACATCG ACCGAGCGCG TGAACAGGTT GAGGCGCTTC CAGTCGCTCT 360
CGCGGTGGCG CAGCAACAGC AGGCTGCCAG TGTTTGCCAT ACCGCGAAGT CTCTCAGCGA 420
CTCCCGCACT CCGCATCGTG GACCAAAATG CCGGAATTCT CCGCGCTCCG CTGCGCAGCG 480
CGTTCATACC GCGGAGGTGG TCGGACCGCT AACGCGCGCT T 521

```

## (2) INFORMATION FOR SEQ ID NO:269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

CTCCAGGCTC ATTGCTCGA ACAAAGCCAC CCGGCGTAC AGCGGACGCC CCCATTGTT 60
GTCTGTATAG TCXCGTACA GCTGGGCATC GGGCCCTGGA CGAACCTCCG CCCAGCGGCA 120
GCGAACCCAG CCGTGGCGCG TCACCGCGGG TCAGAAACGGT AGTGCACGAC AGTCTCGCGG 180
CGCGAAGGCT TTGACCGGTC AGACTCGGCG TCGGCTCTCT CCGACGAGGC GTGGATCGCC 240
CCGAGCTGAG AGCCTAGCGC CTCGAGCTCA CCGCGGAGCT GTTCAGCAC CCAGTCCACT 300
TCGCTGCTCT GTTTCGCGCG CAGCAGCTGC GTGAACCTGA CCGCTCGAC ATCGGCGCGG 360
GTGAGCTTGA ACCCGCGCAG CCGCTCGCGC GTGCTCGCGC GCGGCGGCGG CCGCAACTGC 420
TCGCGA 426

```

## (2) INFORMATION FOR SEQ ID NO:270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

CGCGACACCG CCGACAAGC GCAATCGGCT TCGGCGCGCG CCGCGCGCGC GACCGCGGCG 60
AGGCGCGCGC CCGCGCGCGA CTGTGGGCTA CTGCGCGGCG CCGCGGACAC GCGCGGCGCA 120
GCGCGTGGTA CCGCGCGCGC ACCGCTGCGC GTTCAGGCGC GCATGCGCGC CCGCGGCGCG 180
CGCGGTGGCG TGAATCGGCA CCGCGCGCGC GCGCGCGAC 219

```

## (2) INFORMATION FOR SEQ ID NO:271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

AAGATCATCG GCGCCGCTCC TTAGCATCGC TCGCTCTGCG ATGCTGCGCG GCGCGGATCA      60
CGGAGGTCCG GCGTTGTACC CCACTGCTCG AACGGTCAGC ACCACACTCG GGTTCCTCGG      120
ATCCTTTTTC ACCTTGGCCC GCAGACGCTG GACATGCACG TTCACCGAGC TGTATATCGG      180
TGGGTGCGCG TAACCCGATA CCGTTTCGAG CAGCACATCA CGAGTAAACA CCGCGCCCGG      240
CTTGCGCGCC AATGCGACCA ACGGTTGAA TTCCAGCGGT GTCAACGAGA TCTGCTCACC      300
GTTGCGAGTG ACCTTGTGCG CCGGTACGTC GATTTCTACG TCGGCGATCG ACAGCATCTC      360
GCGCGGTTCG TCGTGGTTGC GCGCGAGCGC CCGCCGACCC CCGCGACCA GCTCCTTGGG      420
CTTGAACGGC TTCATGATGT AGTCGTGCGC GCGCGACTCC AGACCCAGCA CCACATCCAC      480
GCTGTGCGTC TTGCGGTTGA GCATCAGCAT CGGAACACCG GATCGGCGC GCAACACCCG      540
GCACACGTCG ATGCGGTTCA TACCGGGCA A

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala      1
1          5          10          15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly      20
20          25          30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu      35
35          40          45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp      50
50          55          60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly      65
65          70          75          80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
          85          90

```

(3) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro      1
1          5          10          15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro

```

20

25

## (2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1             5             10             15
Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
      20             25

```

## (2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1             5             10             15
His Pro Pro Asn
      20

```

## (2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1             5             10             15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
      20             25             30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
      35             40             45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg

```